

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

## (i) APPLICANTS:

(A) NAME : I.N.S.E.R.M  
(B) STREET : 101, rue de Tolbiac  
(C) CITY : PARIS CEDEX 13  
(E) COUNTRY : FRANCE  
(F) POSTAL CODE (ZIP) : 75654

(A) NAME : Max-Planck-Gesellschaft zur Förderung  
des Wissenschaften e. V., Berlin  
(B) STREET : Hofgartenstrasse 2  
(C) CITY : München  
(E) COUNTRY: Germany  
(F) POSTAL CODE (ZIP) : 80539

(A) NAME : SMITHKLINE BEECHAM  
(B) STREET: New Horizons Court  
(C) CITY : Brentford  
(D) COUNTY: Middlesex  
(E) COUNTRY : Great-Britain  
(F) POSTAL CODE (ZIP) : TW 89 EP

(ii) TITLE OF THE INVENTION: DNA, specific proteins and peptides of the *Neisseria meningitidis* species bacteria, methods for obtaining them and their biological application.

(iii) NUMBER OF SEQUENCES: 99

## (iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (OEB)

## (2) INFORMATION FOR SEQ ID NO: 1:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

## (ii) TYPE DE MOLECULE: DNA (genomic)

## (vi) ORIGIN:

- (A) ORGANISM : Neisseria meningitidis
- (B) STRAIN : Z2491

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GATCCGCTGC CGGCAGACGA ATATCAAGAC ATCTTCGATT TTATGAAACA GTATGACTTG 60  
 TCTTACCCGT ATGAATATCT GCAGGATTGG ATAGATTACT ATACGTTCAA AACCGATAAG 120  
 CTGGTATTTG GTAACGCGAA GCGAGAGTGA GCCGTAAAAC TCTGAGCTCC TGTTTTATAG 180  
 ATTACAAC TT TAGGCCGTCT TAAAGCTGAA AGATTTTCGA AAGCTATAAA TTGAAGCCCT 240  
 TCCACAGTAC ATAGATC 257

## (2) INFORMATION FOR SEQ ID NO: 2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

## (ii) TYPE DE MOLECULE: DNA (genomic)

## (vi) ORIGIN:

(A) ORGANISM : *Neisseria meningitidis*

(B) STRAIN : Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

GATCATGTTT AAATAGATAG GCATGGGAAG CTGCAGCTCT AACGTCCATG AAAATATGTT	60
GCATAGCTGC AAGCGGAACG CCTTTTCTTT CATCTACATA ATCTATAGAG TCAAGGCAAC	120
CGCTATTGAA ATTAGCAGTA TTGCCTATGA TTACATTAGT AATATGCTCA TACCATTTTT	180
GGGTGGTCAT CATATTGTGC CCCATTGTTA TCTCCTTATA TTGGTTTTAG AAGGAACTTT	240
GACAGGAAGA ATAACGGCCT TACCTGTTTG ACGATC	276

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 428 base pairs

(B) TYPE: nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

(A) ORGANISM : *Neisseria meningitidis*

(B) STRAIN : Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GATCTGGTGG TGTTTGCACA GGTAGGCGCA TACTTGTTTCG GGACTGAGTT TGCGGCGGAT	60
AAGGGTGTCG ATGTGCTGAA TCAGCTGCGA ATCGAGCTTA TAGGGTTGTC GCTTACGCTG	120
TTTGATAGTC CGGCTTTGCC GCTGGGCTTT TTCGGCGCTG TATTGCTGCC CTTGGGTGCG	180

T04T03 4542663

GTGCCGTCTG ATTTGCGCGC TGATGGTGCT TTGTGGCGG TTAAGCTGTT TGGCGATTTTC 240  
GGTGACGGTG CAGTGGCGGG ACAGGTATTG GATGTGGTAT CGTTCGCCTT GGGTCAGTTG 300  
CGTGTAGCTC ATGGCAATCT TTCTTGCAGG AAAGGCCGTA TGCTACCGCA TACTGGCCTT 360  
TTTCTGTTAG GGAAAGTTGC ACTTCAAATG CGAATCCGCC GACCTCTTTC AGTTACAGCA 420  
GCTTGATC 428

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM : *Neisseria meningitidis*
- (B) STRAIN : Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

GATCCTGCAT TGACATCGGC CTTGGCTGTC AGGGTATTGT GACCGGTAAA GTCGGCATT 60  
CCGTTGGCCA ATAAGGATAC ATGACCGTCT GCAGAAACAG CATGAAGGCC GTCTGAAACG 120  
ATATTGCCCT GCAATGCGGT GGTTCGAGA GCCTTGGCTG CGTTCAGCTT GGTATTGCGA 180  
AGCTGAATAT TGCCTTTGGC TGCCTGAATG TGCAGATTAC CCGAGTTGGT ACGCAGATTG 240  
GTATTGGTAA CATTAGCAA GCCTGCCTCC ACACCCATGT CTTTGTAGGC AGTGAGGGTT 300  
TTACTGGTGC CGGTAATATG GGCAGCGTTA TCCGATTTC AATGGATGCT GGCCGGCAGA 360

CAAATCTTTA TCAACATTCA AATTCAGATC

390

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM : Neisseria meningitidis
- (B) STRAIN : Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

GATCAGATTG GTGAAGACGG TATTACCGTC AATGTTGCAG GCCGTTCTGGG ATATACGGCG	60
AAAATCGACG TGTCTCCGAG TACCGATTTC GCGGTTTATG GCCATATTGA AGTTGTACGG	120
GGTGCAACGG GGTTGACCCA ATCCAATTCA GAGCCGGGTG GAACCGTCAA TTTGATC	177

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

F04430-4543660

## (vi) ORIGIN:

(A) ORGANISM : *Neisseria meningitidis*

(B) STRAIN : Z2491

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GATCAATGAT GCTACTATTTC AAGCGGGCAG TTCCGTGTAC AGCTCCACCA AAGGCGATAC 60

TGAATTGGGT GAAAATACCC GTATTATTGC TGAAAACGTA ACCGTATTAT CTAACGGTAG 120

TATTGGCAGT GCTGCTGTAA TTGAGGCTAA AGACACTGCA CACATTGAAT CGGGCAAACC 180

GCTTTCTTTA GAAACCTCGA CCGTTGCCTC CAACATCCGT TTGAACAACG GTAACATTAA 240

AGGCGGAAAG CAGCTTGCTT TACTGGCAGA CGATAACATT ACTGCCAAAA CTACCAATCT 300

GAATACTCCC GGCAATCTGT ATGTTCATAC AGGTAAAGAT C 341

## (2) INFORMATION FOR SEQ ID NO: 7:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 164 base pairs

(B) TYPE : nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY : linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGIN:

(A) ORGANISM : *Neisseria meningitidis*

(B) STRAIN : Z2491

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GATCCAACCTG TTTGATTTTA CTGGCTGCTT CTCCATGCGC GGTATTGACC AAAGCCGCAA 60

GGATATTGCG TTCCAGATTG TCTTTCAGGC TGCCGCCGTT GACAGCGGTA TTAATCAGTG 20

T04T30 43422660

CGGCACTGCC CGCATTGGCT AGGTTGACGG TCAGGTTGTT GATC

164

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM : *Neisseria meningitidis*
- (B) STRAIN : Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GATCAATCAC ACATCTTGTC ATTTTTTCGA TTCCTTCATT TCGGTTTCTA ATGTTTCAAT 60  
TCTTGCGGCC ATTTCTTGAA TGGCTTTAGT CAAAACGGGG ATGAACGCTT CGTATTCGAC 120  
GGTGTAGGTA TCGTTTGTTT TATTTACCAT CGGCAATCGA CCATATTCAT CTTCCAGCGC 180  
AGCAATGTCC TGGGCAATAA ACCAATGCCG CAACCGATC 219

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

(A) ORGANISM : *Neisseria meningitidis*

(B) STRAIN : Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GATCTTGGGT AAGCCCCCAA CCTGCATAGA AAGGCAGGCC GTAGCAGCTG ACTTTTTTGC 60  
 CGCGCAACAA GGCTTCAAAA CCGGTCAGCG AAGTCATGGT ATGTATTTTCG TCTGCGTATT 120  
 GGAGACAGGT CAGGATGTCG GCTTGTTTCGG CGGTTTGGTC GGCATATCGT GCAGCATCAT 180  
 CAGGGGAAAT ATGGCCGATG CGGTTACCGC TGA CTACATC GGGATGCGGT TTGTAGATGA 240  
 TATAGGCATT GGGGTTTCGT TCGCGTACGG TACGGAGCAA ATCCAGATTG CGGTAGATTT 300  
 GGGGCGAACC GTAGCGGATA GACGCATCAT CTTCAACCTG GCCGGGAACG AGGATC 356

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 210 base pairs

(B) TYPE : nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

(A) ORGANISM : *Neisseria meningitidis*

(B) STRAIN : Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GATCCGCTTT CAGTTTCCGT ACCGGTGGCA TCAGTCAAGT CCGTTTTGTG CACCAAACCG 60

F04T00" 454B3660



CGTCCATATG AAACATAAAA CAAATCGCTT AAGCCCAAAG GGTATATCGAA CGATAAAGCG 120  
 ACATTTTCCTT GATATTTGCC GGTCGTTTTG CCGCCCGCAT CATCTATACC GATACTGAAC 180  
 CGTATGGGTT TATTCTGCTG CCATTTGATC 210

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM : Neisseria meningitidis
- (B) STRAIN : Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GATCCCGAAA CGCAATTGGT CGAAAGCTAT ATGCTGAACG ATGTGTTGCG GTTTTGGGAC 60  
 AGCGCAGGTT TGGGCGATGG GAAAGAAGCC GACCGCGCCC ATCGGCAGAAA ACTGATTGAT 120  
 GTCCTGTCTA AAACCTATAC TCATTTCGGAT GGGCAGTGGG GCTGGATAGA TTTGGTGTTC 180  
 GTTATCCTTG ACGGCAGCTC CCGCGATTTG GGTACGGCCT ATGATTTGTT GAGGGATGTT 240  
 ATCCTTAAAA TGATTGATC 259

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 436 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single

F04YB04E060

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

(A) ORGANISM : *Neisseria meningitidis*

(B) STRAIN : Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GATCAAATGG ATGATTTATA TAGAATTTTC TTTTACGACT GCGTGCCGTT TGAAAAGAAA	60
ATGCACAATC CCGTATCTCA TCGTGCCATA GATTTTTTCAA AGACTCCGGA AGCCATATTT	120
CGTTGCAATC TGCATACCGA ATTGAAGAAG AAGCGTAAAT TAGCGTTACG TTTAGGCAAG	180
CTGTCGGACA ATACAGCATG GATATTAAAA CCCCAAGTCA TGAAAAATCT TCTGAAAAAC	240
CCGTCAACTC AAATTACGGA AAACGATGTC GTGCTCGATG TTAAACAAA AGGTGTAGAT	300
ATGCGTATAG GCTTGGATAT TTCATCTATT ACCTTAAAAA AACAAGCCGA TAAATCATC	360
TTGTTTTCTG GTGATTCCGA TTTTGTCCCA GCAGCCAAAT TAGCCAGACG GGAAGGTATC	420
GATTTTATTC TTGATC	436

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 363 base pairs

(B) TYPE : nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

F04T03 2342660

(A) ORGANISM : *Neisseria meningitidis*

(B) STRAIN : Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

```

GATCGTTTTA CGTCGCAATC GAGCTTTGTG GTGCGCTCGC CTAAAAGCCA ATCTTCTCTC    60
AATGGCCTGG GTGCCATTTT GCAGGGCACA GGTTTTGCCC GTGCGCAAGA CGATATTTAT    120
ACCGTGCAGG AATATATGCA GTCGCGTTCG GCTTTGGATG CGTTGCGTAA GAAAATGCCC    180
ATTCGCGATT TTTATGAAAA AGAAGGCGAT ATTTTCAGCC GTTTTAATGG TTTTGGCCTG    240
CGTGGCGAGG ATGAGGCGTT TTATCAATAC TACCGTGATA AGGTATCCAT CCATTTTGAC    300
TCTGTCTCAG GCATTTCCAA TTTGAGCGTT ACATCGTTTA ATGCCGGTGA ATCTCAAAG    360
ATC                                                                    363

```

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 314 base pairs

(B) TYPE : nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

(A) ORGANISM : *Neisseria meningitidis*

(B) STRAIN : Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

```

GATCTTGCGT CATTTATATC TTCACCGATA TTGCAATTAC CGCCGTTCCA GTTGAAATAA    60

```

CAACGACTAA AATTGTAGTT CCTAAAAGAA TCATTCTAT TCTTGCCTAC CATTTCCCAA 120  
 TAATTGCGCC CGACAATTC CATTTAATGC TCCATCAGTT CTTTACTTC CGGAAATCTG 180  
 CTGTAATCTG ACATAAGACG CATAATTGAA CTATCAACGC CGTAACAGCC ATAGGTTTTA 240  
 ATACCGTTTT CGGCGTGTT CCAAATGCAA TTAGTGATT CGTAGCCTTT TACAAATTTA 300  
 TCGGTTTCGG GATC 314

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM : Neisseria meningitidis
- (B) STRAIN : Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

GATCATACGA ATCTACCCTA AAATACCCCG TCGCCGATTT AGGATTGGCT ACATAAAGCT 60  
 CATTATAAGG GTATTTTGAT GACATGATAC GGTAAATTC ATTGCCGTTG TTTATCCTGA 120  
 TTCTATAAAT TGGTTCAACA GCAAAGCCTC TGGATTCCCT TAATTGATTA TAATATTGCC 180  
 TGTATGTTTG TACATCATGT CTTGTCCACG GCTCTCCAGG AGTCCTCAGA ATAGCAATCC 240  
 CGTTAAATTT CGGATC 256

## (2) INFORMATION FOR SEQ ID NO: 16:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGIN:

- (A) ORGANISM : Neisseria meningitidis
- (B) STRAIN : Z2491

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

GATCCACGCC TGTGCCTACC TTGGCTTTTT GTTCGCCAAA CAAGGCATTT AAGGTTGAGG 60

ACTTGCCGAC ACCTGTCGCA CCGACAAGCA AGACATCCAA ATGACGGAAA CCGGCTGCTG 120

TGACTTTTTTG CCCGATTTC AAAATACGGT AACGATGCAT ATGCGCTCCT ACCAGCCAAA 180

AAAAGAAGCA ACCGTGCTAA TCGCCCCTCC AATCGCTTTT GCAGCACCGC CGATC 235

## (2) INFORMATION FOR SEQ ID NO: 17:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGIN:

- (A) ORGANISM : Neisseria meningitidis
- (B) STRAIN : Z2491

F04T030 4343260

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

GATCCAACGG GCATCGCTGT CCTTACTCGG TGTGGTTTGA CCGCTGATTT GTCCTTCTTC 60  
 GTCAACTTCT ATGGCCTGAC GCTGTTTGCT GCCGGCGGTC TGGATAATGG TGGCATCAAC 120  
 GACGGCGGCG GATGCTTTCT CTATTTTITAG GCCTTTTTCG GTCAGTTGGC AGTTAATCAG 180  
 TTTGAGTAAT TCGGACAGGG TGTCGTCTTG CGCCAGCCAG TTGCGGTAGC GGCATAAGGT 240  
 ACTGTAATCG GGGATGATC 259

## (2) INFORMATION FOR SEQ ID NO: 18:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGIN:

- (A) ORGANISM : Neisseria meningitidis
- (B) STRAIN : Z2491

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

GATCTGTGCC GTTGATTTTA TCTTTCAGAT GCAGCATCGA ATATCGGAAA GCCAAATCAG 60  
 CAATTCTTTT TGCATCGTGT GGATTTTGAG ACGGGCCTAA TGACCGTACC CGCTTAATAA 120  
 AAAATGCACC GTCAATCAAA ATGGCGGTTT TCATATTGCT TCCCCTATAT TTGTCAAAGA 180  
 TATAAAAAAG CCCTTGGGAT C 201

T04T03 2348660

## (2) INFORMATION FOR SEQ ID NO: 19:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGIN:

- (A) ORGANISM : Neisseria meningitidis
- (B) STRAIN : Z2491

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

AATTCAAAGG AGGCATTTGT TGCAAGAAAA GTACAAAGTG ATTTGCAAAA AGCATTGAAT 60  
 GCTAGCAACT ATAACAAGCA GCAATATGCA AGACGTGCGG CAACAGCGTT AGAGAATGCT 120  
 TCAAAATCAA AAGTTATGGC AGCGAATTCT TTTTGATCTA TCTTGTGCGA ACGGGTCAAA 180  
 TATTCITCGT ACATTGAGTT AATCGTACCA ATCGCCCTAA CCACATTTTC ATCAGAAAAT 240  
 ATGGAAATAA TAGCATCCCT ATACGCACCT AGTGTAATAT TGTTTCTATT ATTAGTTATA 300  
 GCATTATTCG AATACATAAT AGCACCTCCA AATT 334

## (2) INFORMATION FOR SEQ ID NO: 20:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

## (ii) MOLECULE TYPE: DNA (genomic)

F049330-4342653

## (vi) ORIGIN:

- (A) ORGANISM : *Neisseria meningitidis*  
 (B) STRAIN : Z2491

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

AATTCCTGCG CACCTTTGCC GATGGGGAGA TAATCGCCTT TTTGCAGCAT TCTGCCCTGA 60  
 TGGCCGCCGA AACCGGCTTT CAGGTCGGTA CTTCTCGAAC CCATCACTTC CGGCACATCA 120  
 AATCCGCCCCG CCACGCACAC ATAGCCGTAC ATGCCCTGCA CGGCACGCAC CAGTTTCAAG 180  
 GTCTGCCCTT TCGGGCGGT ATAACGCCAA TACGAATAGA CCGGTTTCGCC GTCCAATT 238

## (2) INFORMATION FOR SEQ ID NO: 21:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs  
 (B) TYPE : nucleotide  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY : linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGIN:

- (A) ORGANISM : *Neisseria meningitidis*  
 (B) STRAIN : Z2491

## (xi) DESCRIPTION DE LA 4SEQUENCE: SEQ ID NO: 21:

AATTGGGCGA GATGCTGCCG GAAACGGATT TAAAACAGAT TCGGGCGGCA GTGTTGAAGA 60  
 CGAACGATGA GCGGGCATTG CAGAAGGTGG TGAAAACGGC CAAAGGCAAT GCGCGGAAAC 120  
 TGTCGAAGCT GCTGCTGATT GTGGACTATT TGTTGCAGGT TAACCCTGAT GTTGATTGG 180



ATGATGATGT AATCGAACAC GCGGAAACCT ATTTAATCCA CTAAACCTTT GACAGATAAG 240  
GCAATAATT 249

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM : Neisseria meningitidis
- (B) STRAIN : Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

AATTTATGTA CGGTTTTGCC GTTTGCAGTC AGCCAGTCGG CAAGGCGCAG AAAAAAATCG 60  
CCGACAGGGC CTTGAAGCAG CAGGATATTT TCTGCGCTTT CAAGCAGGTT TTGCAGGTTA 120  
TTTTTGAGGA CGGTCTGTTT CATGTTGCAA TGTGGTTTTG TTTTTTATGT AATAGTTTTA 180  
GGTTGAACTT TCAAGCATAC GCCAAGAGAA TT 212

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

(A) ORGANISM : Neisseria meningitidis

(B) STRAIN : Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

```

AATTCAGTGC CTGCGTCATA TCACGGCTAC CTTGTGGTTC AGGGTTACTG TATCGCCCCG 60
GGCATCGACG GCTTCAATAT GCAGCTTCAG CCAGCCGTGC TCGGGGGCGG ATCGGGTTAC 120
TTGGATGGAT TGGGCGCGTT TGGACTGAAT CACGGGCTGC AAGGCTTGCT CGGCGTACTG 180
TTTGGCCAGT ACTTCGATGC GCTTTAAATG CTTTGGCGG CGCAATT 227

```

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 167 base pairs

(B) TYPE : nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

(A) ORGANISM : Neisseria meningitidis

(B) STRAIN : Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

```

GATCCAGGAC TCAAAAACCG ATTTCCTAAT AGAGTGTCTA ATATCCCAAT CTTTTTTACC 60

```

F044304360

CCCTCTGCTG TAGAATTGAT AGAGAAAGTT TGTCTATCTT TTTCATATAC CCATGCCCTTC 120

TTTTTATCAT TGTAGCTAAC ATAACCGCCA AACAATGCTT CTAGATC 167

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM : Neisseria meningitidis
- (B) STRAIN : Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

AATTCCTTGCG GCCATTCCTT GAATGGCTTT AGTCAAAACG GGGATGAACG TTTCGTATTC 60

GACGGTGTAG GTATCGTTTG TTTTATTTAC CATCGGCAAT CGACCATATT CATCTTCCAG 120

CGCAGCAATG TCCTGGGCAA TAAACCAATG CCGCAACCGA TCTTCTTTAT GACTGCCGTC 180

CTTGATTGGA TTCGCCCACC ATTCGCGGAC TTTGTCCGCT CGTTCATCTG CCGGCAAGTC 240

TTTGAATAAT T 251

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs

F04T39 4542663

- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM : Neisseria meningitidis
- (B) STRAIN : Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

```

AATTCCCGAC TATCGCGGAT GCGTAGTTTT TGCCGGTGGG CAAGAGCAGG TGTGGGATAA      60
GTTAGGTGAT TTGCCCCGATG GCGTCAGCCT GACCCCGCCT GAATCGGTAA ATATTGACGG      120
CTTAAAATCC GTAAAACTCG TCGCATTAAA TGCTGCCGCT CAGGCTTTTA TTAACAAGCA      180
CGCCGGTATC GACAGCGTAC CTGAATT                                           207

```

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM : Neisseria meningitidis
- (B) STRAIN : Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

F04T03.03443.03443.03443

AATTGTTTGG GAATAATCCA AACAAACAGC ATCAGGATAG CGGCGGCGGT CAGGCTGCCT 60  
 GAAAGGATTT TGCCGGGGTT TTTTGTAGGC AAAGCGGACG AGAAACCAA GCAACAGCAG 120  
 CATGGTGTCC CAATAGCCGA TTGAGAATAG GATGGCCAAA CCTTCTAGGA AATGGCGTAA 180  
 ATCGTTTGTG GTAACCATGG GTAGTTCCTG TGGTTAAATG TGCAGGCTGC TTTTGTCCGA 240  
 ACCTTGCCGC ATCTCAAAAAG CAGCCTGCGC TTCAGCGTTG CGTTACGCAG TAAATAATG 300  
 AATATTTGTA ACGGCTTGGG TATTTTTTGT CAATATTCCC GCCCTTCCCT TAACAGCTGC 360  
 CGCGCTTTCC GTTAAAATT 379

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM : Neisseria meningitidis
- (B) STRAIN : Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

AATTCGCCGA AATCAGGCTG CTGCTCGATA ATCGGCGCGG CCGATTGGCG TTGTGCCTCG 60  
 ATTAAATCCA TCTTGTCTTG CAGACGTTTG GCCTGGCCTT TGCGGCGGCG TTCGGCCAGT 120  
 TGTTCATCC GCGTTTCCGC AAATGCCGCC CGTTTGTGTC CGTTGAATAC CGCTTTGCAA 180  
 ATCACCTTGC CCTGCATATC CTTACAATC ACATGGTCGG CATCGTGGAT GTCGTAAGCC 240

ACCCGTACCT TCTGACCGCT GTAATCCAGC AATT

274

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM : Neisseria meningitidis
- (B) STRAIN : Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

AATTCCGTTT	TTATTGGGCT	TTTCCATCC	ATCGGGTATG	CCTGAAGGGA	ACGCAAACCC	60
TGCCACTTGC	CCATCGCTCC	ATTCCCGCAT	TAGCGCGTCT	GACGGCAAGT	GTTCTCGCGC	120
CCAATCAAGC	CACGCCTGCC	GCATTGCGGC	CTTGTCTTGC	TGAAAACTTC	GCAGTGCTTT	180
TGCAACCGGC	CCATCATTAA	CTTCAATCAA	ATAAATCATT	ATATTTGCGT	TCATTTTTTC	240
TACACCTTCG	CCACATCCAA	ATT				263

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

(A) ORGANISM : *Neisseria meningitidis*

(B) STRAIN : Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

```

AATTGTTCAA GAAAAAAGTC GGCACGGCGC GGCAACGGGG AAAATGCGTT GACGCCGTCT    60
TTTTCTAAGG TGATGTAGTA GGGGCGGAAA TAGCCTTCTT CAAACGCCCA GAAACTGGCT    120
TGGTTTTTCGT TTGCAATGCG TTTTGCAATG ACGTGATAAG GCGGTGTGTC GCCAAAGCAG    180
ACAACGGCCT GGATGTGATG TTGAGTGATG TATTCTTGCA AAAACTCAGG AAAGGCGTCG    240
TAGTTGTCGT TAAAAACAAC GGTATGCGCT TGAGTGGGCG GATAAAAATA GTCGTCGCCT    300
GCATTAAAGT TGAATT                                                    316

```

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 324 base pairs

(B) TYPE : nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

(A) ORGANISM : *Neisseria meningitidis*

(B) STRAIN : Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

F04789-2491-0904

AATTCAATCA ACGGAAAACA CATCAGCATC AAAACAACG GTGGTAATGC CGACTTAAAA 60  
 AACCTTAACG TCCATGCCAA AAGCGGGGCA TTGAACATTC ATTCCGACCG GGCATTGAGC 120  
 ATAGAAAATA CCAAGCTGGA GTCTACCCAT AATACGCATC TTAATGCACA ACACGAGCGG 180  
 GTAACGCTCA ACCAAGTAGA TGCCTACGCA CACCGTCATC TAAGCATTAC CGGCAGCCAG 240  
 ATTTGGCAAA ACGACAAACT GCCTTCTGCC AACAACTGG TGGCTAACGG TGTATTGGCA 300  
 CTCAATGCGC GCTATTCCCA AATT 324

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM : Neisseria meningitidis
- (B) STRAIN : Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

AATTATGCAA AAAAACGCAA CGCCGAAAAA CTGGCACCGC GCGGATATTG TTGCTGCTTT 60  
 GAAAAAGAAA GGCTGGTCAC TTCGAGCACT TTCAATAGAA GCGGGGTTGT CGCCGAATAC 120  
 GCTTAGAAGC GCACTGGCCG CCCCTTATCT TAAGGGAGAA AGGATTATTG CCGCTGCAAT 180  
 CGGAGTGGAA CCGGAAGAGA TTTGGTCCGA ACGGTATGCA GATCGGAATT 230



## (2) INFORMATION FOR SEQ ID NO: 33:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGIN:

- (A) ORGANISM : Neisseria meningitidis
- (B) STRAIN : Z2491

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

```

AATTTAATCG GTGGAATGCC TGTTCAACCG CACCAATCCC GCTGAATACG GTTGCTAATC    60
TAATATGTGA ATCAGGTTTA AGAAAAGTTT TAGATTTCCA ACCTTGTTGA CTGGGAAAGA    120
GCAAAGTTTT TTGTAATCGA GTATCGTGTG TCTGTGCCAT TGTCGAAATA GTCATACTTA    180
TATCGTTCTG TTTATCTTAT CAATATGAAA ACTACATCGT TGATTGCCCT GACAATGCCT    240
TGGTCAATT                                         249

```

## (2) INFORMATION FOR SEQ ID NO: 34:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

## (ii) MOLECULE TYPE: DNA (genomic)

F04T33 2492663

## (vi) ORIGIN:

(A) ORGANISM : *Neisseria meningitidis*

(B) STRAIN : Z2491

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

AATTCTTGTC CCGGAGTCCA ACGTATATTT ACCCTCCTGC GAGCTAAAAG ACTATTATTC 60  
 TCCACTGCCA CAGTAGCCGC ATTACCGCC GTATTCACAT CCCCTTTAAC CAATGCCACT 120  
 GCGCTGCCTG CGATAATCTG CGAGTAGGCT ATGACTTTTTT GCGCTTCTTG GGGTGACAGT 180  
 TTGCCTACAT CGCGTCCGTC CAACAGGGTT TCTCCCACCA TCTCGCCGAC TGCCGCGCCG 240  
 ATTGCGCCGT CCCGACATTT GCCTTTATTT GCTACCGCCG ATGCACAGCC TGCTACGGCA 300  
 TGGGCTATCT TGTGGGCAAT GTAGTCTTCG CTGAGATTAA ATT 343

## (2) INFORMATION FOR SEQ ID NO: 35:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 184 base pairs

(B) TYPE : nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY : linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGIN:

(A) ORGANISM : *Neisseria meningitidis*

(B) STRAIN : Z2491

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

AATTCTTCAA ACATCGTTTC GATAATCGGG TCGGTGTACA CACTGATGCG GTCGCCCCGA 60

F04T00 4542660

CGGCTTTGAC CGGCTCGGAA AATATAGGCG GTGGCTTTGC CGTCGGCGAT GTCGACGCAC 120  
 CAACGCCAGA TGGCGTCTTC GGTATTCAAA CAATCACCCG CACAGCTTTC ACCTGCGCGG 180  
 AATT 184

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15620 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGIN:

- (A) ORGANISM : Neisseria meningitidis
- (B) STRAIN : Z2491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

TATGCTCAAT CTCATTTTCA AAATGCAAAA CTTTCTGAT TTTTCCTACT TTTTGCTCAA 60  
 TATTAGGAAG GTTTTAGGCA ATTGAAAATT TTTTGGCGCA TTTTATGCG TCAAATTTTCG 120  
 TTAACAGACT ATTTTGTCAA AGGTCTCCGT CTGTAAAAGC AAGGATAGGG CATCTGCCCT 180  
 TTTGATTGTT TGATTAAACGA TACAAGGAGT TTCAAAATGA GAGTTTATA GTGGATTAAAC 240  
 AAAAACCAGT ACAGCGTTGC CTCGCCTTGC CGTACTATTT GTACTGTCTG CGGCTTCGTC 300  
 GCCTTGTCCT GATTAAATTA TAATCCACTA TATGTGTTCA TGAAATGACT TGGGTCGGAG 360  
 GCTCAGGTAA TGCGCAACAA AGTTCATATT ATTGCGAAAT TTGCGAATCT GCAGGGCTTA 420  
 ACGATACGGG AAATCCTGAT AAATCTTTAG GATTGCCAAA CAATACGTTC AGTAATCCGC 480

CTGGTTGGGG AGCTACAATC GGAGCTTTAG CAGGTAGCCG CATAGGTATG CCTGAATTTG 540  
 GTACGTTTGC GAGCCATGCC ATTGAAAATT TCGACTGGTC ATGGTATCGA CGTTATAGGG 600  
 AAATTGCCGA AACGATTGAA CGAGAATATT CAGGCGGTTT GCCTTAATAG TTGAGGAGGT 660  
 CATGATGTTT GCCAAACATT ATCAATTCAT CGCACTCGGC ATCATGCTGC TTCTTTATAT 720  
 GTTGATTCTC TATACGACCG ATTTTTCCTAA TCTGACGTAT TGGATGCTGT TTTTATCTG 780  
 TTTTATTACA GGAAAAATAT TAGCTCGTTT GTTAGAGAAA AGCTTTAAAT AAAATAGCAG 840  
 CTAGTCGCAA AAGGTCGTCT GAAACCTTTT CAGGCGGCCT TTCTAAAATA CATCCAACTT 900  
 CCTAATCCCT ATTTTTCAAA AAGGAAATCT ATGCCCCATC TGCAAAACCT GTCTTTGGGC 960  
 TTAAAGAAAA AGCTGCCTGT TATCCTGCAA ACAGAAATAT CAGAATGCGG CTTGGCATGT 1020  
 CTGGCGGCTG TGGCGGGATT TCATGGTTTC CATA CGAATT TACGCGCACT GCGTTCAAAA 1080  
 TACTGTCCGA GACCTTTGCA AAATCCCCA AAATCCCCTA AATGTCTTGG TGGGAATTTT 1140  
 GGGGAATTTT GCAAAGGTCT CATTCTATAA CTGTAAATAC TTTTAAATTT ATGACAAAAT 1200  
 AGTAAATATT GCTAAAATAA TATTGATGTC ATGAAATTTT TTCTGCTCC ATGTCTGTTG 1260  
 GTTATCCTGG CTGTCATACC CCTTAAAACC TTAGCTGCCG ATGAAAACGA TGCAGAACTT 1320  
 ATCCGTTCCA TGCAGCGTCA GCAGCACATA GATGCTGAAT TGTTAACTGA TGCAAATGTC 1380  
 CGTTTCGAGC AACCATTGGA GAAGAACAAT TATGTCCTGA GTGAAGATGA AACACCGTGT 1440  
 ACTCGGGTAA ATTACATTAG TTTAGATGAT AAGACGGCGC GCAAATTTTC TTTTCTTCCT 1500  
 TCTGTGCTCA TGAAAGAAAC AGCTTTTAAA ACTGGGATGT GTTTAGGTTT CAATAATTTG 1560

AGCAGGCTAC	AAAAAGCCGC	GCAACAGATA	CTGATTGTGC	GTGGCTACCT	CACTTCCCAA	1620
GCTATTATCC	AACCACAGAA	TATGGATTCTG	GGAATTCTGA	AATTACGGGT	ATCAGCAGGC	1680
GAAATAGGGG	ATATCCGCTA	TGAAGAAAAA	CGGGATGGGA	AGTCTGCCGA	GGGCAGTATT	1740
AGTGCATTCA	ATAACAAATT	TCCCTTATAT	AGGAACAAAA	TTCTCAATCT	TCGCGATGTA	1800
GAGCAGGGCT	TGGA AACCT	GCGTCGTTTG	CCGAGTGTTA	AAACAGATAT	TCAGATTATA	1860
CCGTCCGAAG	AAGAAGGCAA	AAGCGATTTA	CAGATCAAAT	GGCAGCAGAA	TAAACCCATA	1920
CGGTTTCAGTA	TCGGTATAGA	TGATGCGGGC	GGCAAAACGA	CCGGCAAATA	TCAAGGAAAT	1980
GTCGCTTTAT	CGTTCGATAA	CCCTTTGGGC	TTAAGCGATT	TGTTTTATGT	TTCATATGGA	2040
CGCGGTTTGG	TGCACAAAAC	GGACTTGACT	GATGCCACCG	GTACGGAAAC	TGAAAGCGGA	2100
TCCAGAAGTT	ACAGCGTGCA	TTATTCGGTG	CCCGTAAAAA	AATGGCTGTT	TTCTTTTAAT	2160
CACAATGGAC	ATCGTTACCA	CGAAGCAACC	GAAGGCTATT	CCGTCAATTA	CGATTACAAC	2220
GGCAACAAT	ATCAGAGCAG	CCTGGCCGCC	GAGCGCATGC	TTTGGCGTAA	CAGGTTTCAT	2280
AAAAC TTCAG	TCGGAATGAA	ATTATGGACA	CGCCAAACCT	ATAAATACAT	CGACGATGCC	2340
GAAATCGAAG	TGCAACGCCG	CCGCTCTGCA	GGCTGGGAAG	CCGAATTGCG	CCACCGTGCT	2400
TACCTCAACC	GTTGGCAGCT	TGACGGCAAG	TTGTCTTACA	AACGCGGGAC	CGGCATGCGC	2460
CAAAGTATGC	CCGCACCTGA	AGAAAACGGC	GGCGGTACTA	TTCCAGGCAC	ATCCCGTATG	2520
AAAATCATAA	CCGCCGGATT	GGATGCAGCG	GCCCCGTTTA	TGTTGGGCAA	ACAGCAGTTT	2580
TTCTACGCAA	CCGCCATTCA	AGCTCAATGG	AACAAAACGC	CTTTGGTTGC	CCAAGACAAG	2640
TTGTCTATCG	GCAGCCGCTA	CACCGTTCGC	GGATTTGATG	GGGAGCAGAG	TCTTTTCGGA	2700

GAGCGAGGTT TCTACTGGCA GAATACTTTA ACTTGGTATT TTCATCCGAA CCATCAGTTC	2760
TATCTCGGTG CGGACTATGG CCGCGTATCT GGCAGAAAGTG CACAATATGT ATCGGGCAAG	2820
CAGCTGATGG GTGCAGTGGT CGGCTTCAGA GGAGGGCATA AAGTAGGCGG TATGTTTGCT	2880
TATGATCTGT TTGCCGGCAA GCCGCTTCAT AAACCCAAAG GCTTTCAGAC GACCAACACC	2940
GTTTACGGCT TCAACTTGAA TTACAGTTTC TAACCTCTGA ATTTTTTTAC TGATATTTAG	3000
ACGGTCTTTC CTTATCCTCA GACTGTCAAA CTTTACCTAC GTACTTGGCG CGCAGTACGT	3060
TCATCTTCAA AATGGAATAG ACATGAATAA AGGTTTACAT CGCATTATCT TTAGTAAAAA	3120
GCACAGCACC ATGGTTGCAG TAGCCGAAAC TGCCAACAGC CAGGGCAAAG GTAAACAGGC	3180
AGGCAGTTCG GTTTCTGTTT CACTGAAAAC TTCAGGCGAC CTTTGCGGCA AACTCAAAAC	3240
CACCCTTAAA ACCTTGGTCT GCTCTTTGGT TTCCCTGAGT ATGGTATTGC CTGCCCATGC	3300
CCAAATTACC ACCGACAAAT CAGCACCTAA AAACCAGCAG GTCGTTATCC TTAAAACCAA	3360
CACTGGTGCC CCCTTGGTGA ATATCCAAAC TCCGAATGGA CGCGGATTGA GCCACAACCG	3420
CTATACGCAG TTTGATGTTG ACAACAAAGG GGCAGTGTTA AACAACGACC GTAACAATAA	3480
TCCGTTTCTG GTCAAAGGCA GTGCGCAATT GATTTTGAAC GAGGTACGCG GTACGGCTAG	3540
CAAACCTAAC GGCATCGTTA CCGTAGGCGG TCAAAAGGCC GACGTGATTA TTGCCAACCC	3600
CAACGGCATT ACCGTTAATG GCGGCGGCTT TAAAAATGTC GGTCTGGGGCA TCTTAACTAT	3660
CGGTGCGCCC CAAATCGGCA AAGACGGTGC ACTGACAGGA TTTGATGTGC GTCAAGGCAC	3720
ATTGACCGTA GGAGCAGCAG GTTGGAATGA TAAAGGCGGA GCCGACTACA CCGGGGTACT	3780

TGCTCGTGCA GTTGCTTTGC AGGGGAAATT ACAGGGTAAA AACCTGGCGG TTTCTACCGG	3840
TCCTCAGAAA GTAGATTACG CCAGCGGCGA AATCAGTGCA GGTACGGCAG CGGGTACGAA	3900
ACCGACTATT GCCCTTGATA CTGCCGCACT GGGCGGTATG TACGCCGACA GCATCACACT	3960
GATTGCCAAT GAAAAAGGCG TAGGCGTCAA AAATGCCGGC AACTCGAAG CGGCCAAGCA	4020
ATTGATTGTG ACTTCGTCAG GCCGCATTGA AAACAGCGGC CGCATCGCCA CCACTGCCGA	4080
CGGCACCGAA GCTTCACCGA CTTATCTCTC CATCGAAACC ACCGAAAAAG GAGCGGCAGG	4140
CACATTTATC TCCAATGGTG GTCGGATCGA GAGCAAAGGC TTATTGGTTA TTGAGACGGG	4200
AGAAGATATC AGCTTGCGTA ACGGAGCCGT GGTGCAGAAT AACGGCAGTC GCCCAGCTAC	4260
CACGGTATTA AATGCTGGTC ATAATTTGGT GATTGAGAGT AAAACTAATG TGAACAATGC	4320
CAAAGGCTCG GCTAATCTGT CGGCCGGCGG TCGTACTACG ATCAATGATG CTACTATTCA	4380
AGCGGGCAGT TCCGTGTACA GCTCCACCAA AGGCGATACT GAATTGGGTG AAAATACCCG	4440
TATTATTGCT GAAAACGTAA CCGTATTATC TAACGGTAGT ATTGGCAGTG CTGCTGTAAT	4500
TGAGGCTAAA GACACTGCAC ACATTGAATC GGGCAAACCG CTTTCTTTAG AAACCTCGAC	4560
CGTTGCCTCC AACATCCGTT TGAACAACGG TAACATTAAA GCGGGAAGC AGCTTGCTTT	4620
ACTGGCAGAC GATAACATTA CTGCCAAAAC TACCAATCTG AATACTCCCG GCAATCTGTA	4680
TGTTCATACA GGTAAGATC TGAATTTGAA TGTGATAAA GATTTGTCTG CCGCCAGCAT	4740
CCATTTGAAA TCGGATAACG CTGCCCATAT TACCGGCACC AGTAAACCC TCACTGCCTC	4800
AAAAGACATG GGTGTGGAGG CAGGCTTGCT GAATGTTACC AATACCAATC TCGGTACCAA	4860
CTCGGGTAAT CTGCACATTC AGGCAGCCAA AGGCAATATT CAGCTTCGCA ATACCAAGCT	4920

GAACGCAGCC AAGGCTCTCG AAACCACCGC ATTGCAGGGC AATATCGTTT CAGACGGCCT	4980
TCATGCTGTT TCTGCAGACG GTCATGTATC CTTATTGGCC AACGGTAATG CCGACTTTAC	5040
CGGTCACAAT ACCCTGACAG CCAAGGCCGA TGTCAATGCA GGATCGGTTG GTAAAGGCCG	5100
TCTGAAAGCA GACAATACCA ATATCACTTC ATCTTCAGGA GATATTACGT TGGTTGCCGG	5160
CAACGGTATT CAGCTTGGTG ACGGAAAACA ACGCAATTCA ATCAACGGAA AACACATCAG	5220
CATCAAAAAC AACGGTGGTA ATGCCGACTT AAAAAACCTT AACGTCCATG CCAAAGCGG	5280
GGCATTGAAC ATTCAITCCG ACCGGGCATT GAGCATAGAA AATACCAAGC TGGAGTCTAC	5340
CCATAATACG CATCTTAATG CACAACACGA GCGGGTAACG CTCAACCAAG TAGATGCCTA	5400
CGCACACCGT CATCTAAGCA TTACCGGCAG CCAGATTTGG CAAAACGACA AACTGCCTTC	5460
TGCCAACAAG CTGGTGGCTA ACGGTGTATT GGCACTCAAT GCGCGCTATT CCCAAATTGC	5520
CGACAACACC ACGCTGAGAG CGGGTGCAAT CAACCTTACT GCCGGTACCG CCCTAGTCAA	5580
GCGCGGCAAC ATCAATTGGA GTACCGTTTC GACCAAGACT TTGGAAGATA ATGCCGAATT	5640
AAAACCATTG GCCGGACGGC TGAATATTGA AGCAGGTAGC GGCACATTAA CCATCGAACC	5700
TGCCAACCGC ATCAGTGCGC ATACCGACCT GAGCATCAAA ACAGGCGGAA AATTGCTGTT	5760
GTCTGCAAAA GGAGGAAATG CAGGTGCGCC TAGTGCTCAA GTTTCCTCAT TGGAAGCAAA	5820
AGGCAATATC CGTCTGGTTA CAGGAGAAAC AGATTTAAGA GGTTCTAAAA TTACAGCCGG	5880
TAAAACTTG GTTGTGCGCA CCACCAAAGG CAAGTTGAAT ATCGAAGCCG TAAACAACCTC	5940
ATTCAGCAAT TATTTTCCTA CACAAAAAGC GGCTGAACTC AACCAAAAAT CCAAAGAATT	6000



GGAACAGCAG ATTGCGCAGT TGAAAAAAG CTCGCCTAAA AGCAAGCTGA TTCCAACCCT	6060
GCAAGAAGAA CGCGACCGTC TCGCTTTCTA TATTCAAGCC ATCAACAAGG AAGTTAAAGG	6120
TAAAAAACC AAAGGCAAAG AATACCTGCA AGCCAAGCTT TCTGCACAAA ATATTGACTT	6180
GATTTCCGCA CAAGGCATCG AAATCAGCGG TTCCGATATT ACCGCTTCCA AAAAAGTAA	6240
CCTTCACGCC GCAGGCGTAT TGCCAAAGGC AGCAGATTCA GAGGCGGCTG CTATTCTGAT	6300
TGACGGCATA ACCGACCAAT ATGAAATTGG CAAGCCCACC TACAAGAGTC ACTACGACAA	6360
AGCTGCTCTG AACCAAGCCTT CACGTTTGAC CGGACGTACG GGGGTAAGTA TTCATGCAGC	6420
TGCGGCACTC GATGATGCAC GTATTATTAT CGGTGCATCC GAAATCAAAG CTCCCTCAGG	6480
CAGCATAGAC ATCAAAGCCC ATAGTGATAT TGTAAGGAG GCTGGACAAA ACGATGCCTA	6540
TACCTTCTTA AAAACCAAAG GTAAAAGCGG CAAAATCATC AGAAAAACCA AGTTTACCAG	6600
CACCCGCGAC CACCTGATTA TGCCAGCCCC CGTCGAGCTG ACCGCCAAG GTATCAGCT	6660
TCAGGCAGGC GGCAACATCG AAGCTAATAC CACCCGCTTC AATGCCCTG CAGGTAAAGT	6720
TACCCTGGTT GCGGGTGAAG AGCTGCAACT GCTGGCAGAA GAAGGCATCC ACAAGCACGA	6780
GTTGGATGTC CAAAAAGCC GCCGCTTTAT CGGCATCAAG GTAGGTAAGA GCAATTACAG	6840
TAAAAACGAA CTGAACGAAA CCAAATTGCC TGTCCGCGTC GTCGCCCAA CTGCAGCCAC	6900
CCGTTCAAGC TGGGATACCG TGCTCGAAGG TACCGAATTC AAAACCACGC TGGCCGGTGC	6960
CGACATTCAG GCAGGTGTAG GCGAAAAAGC CCGTGTCGAT GCGAAAATTA TCCTCAAAGG	7020
CATTGTGAAC CGTATCCAGT CGGAAGAAAA ATTAGAAACC AACTCAACCG TATGGCAGAA	7080
ACAGGCCGGA CGCGGCAGCA CTATCGAAAC GCTAAAGTGG CCCAGCTTCG AAAGCCCTAC	7140

TCCGCCCAAA	TTGTCCGCAC	CCGGCGGCTA	TATCGTCGAC	ATTCCGAAAG	GCAATCTGAA	7200
AACCGAAATC	GAAAAGCTGT	CCAAACAGCC	CGAGTATGCC	TATCTGAAAC	AGCTCCAAGT	7260
AGCGAAAAAC	ATCAACTGGA	ATCAGGTGCA	GCTTGCTTAC	GACAGATGGG	ACTACAAACA	7320
GGAGGGCTTA	ACCGAAGCAG	GTGCGGCGAT	TATCGCACTG	GCCGTTACCG	TGGTCACCTC	7380
AGGCGCAGGA	ACCGGAGCCG	TATTGGGATT	AAACGGTGCG	GCCGCCGCCG	CAACCGATGC	7440
AGCATTCGCC	TCTTTGGCCA	GCCAGGCTTC	CGTATCGTTC	ATCAACAACA	AAGGCGATGT	7500
CGGCAAAACC	CTGAAAGAGC	TGGGCAGAAG	CAGCACGGTG	AAAAATCTGG	TGGTTGCCGC	7560
CGCTACCGCA	GGCGTAGCCG	ACAAAATCGG	CGCTTCGGCA	CTGAACAATG	TCAGCGATAA	7620
GCAGTGGATC	AACAACCTGA	CCGTCAACCT	AGCCAATGCG	GGCAGTGCCG	CACTGATTAA	7680
TACCGCTGTC	AACGGCGGCA	GCCTGAAAGA	CAATCTGGAA	GCGAATATCC	TTGCGGCTTT	7740
GGTCAATACC	GCGCATGGAG	AAGCAGCCAG	TAAAATCAAA	CAGTTGGATC	AGCACTACAT	7800
AGTCCACAAG	ATTGCCCATG	CCATAGCGGG	CTGTGCGGCA	GCGGCGGCGA	ATAAGGGCAA	7860
GTGTCAGGAT	GGTGCGATAG	GTGCGGCTGT	GGGCGAGATA	GTCGGGGAGG	CTTTGACAAA	7920
CGGCAAAAAT	CCTGACACTT	TGACAGCTAA	AGAACGCGAA	CAGATTTTGG	CATACAGCAA	7980
ACTGGTTGCC	GGTACGGTAA	GCGGTGTGGT	CGGCGGCGAT	GTAAATGCGG	CGGCGAATGC	8040
GGCTGAGGTA	GCGGTGAAAA	ATAATCAGCT	TAGCGACAAA	GAGGGTAGAG	AATTTGATAA	8100
CGAAATGACT	GCATGCGCCA	AACAGAATAA	TCCTCAACTG	TGCAGAAAAA	ATACTGTAAA	8160
AAAGTATCAA	AATGTTGCTG	ATAAAAGACT	TGCTGCTTCG	ATTGCAATAT	GTACGGATAT	8220

ATCCCGTAGT ACTGAATGTA GAACAATCAG AAAACAACAT TTGATCGATA GTAGAAGCCT	8280
TCATTCATCT TGGGAAGCAG GTCTAATTGG TAAAGATGAT GAATGGTATA AATTATTCAG	8340
CAAATCTTAC ACCCAAGCAG ATTTGGCTTT ACAGTCTTAT CATTTGAATA CTGCTGCTAA	8400
ATCTTGGCTT CAATCGGGCA ATACAAAGCC TTTATCCGAA TGGATGTCCG ACCAAGGTTA	8460
TACACTTATT TCAGGAGTTA ATCCTAGATT CATTCCAATA CCAAGAGGGT TTGTAAAACA	8520
AAATACACCT ATTACTAATG TCAAATACCC GGAAGGCATC AGTTTCGATA CAAACCTAAA	8580
AAGACATCTG GCAAATGCTG ATGGTTTTAG TCAAGAACAG GGCATTAAAG GAGCCCATAA	8640
CCGCACCAAT TTTATGGCAG AACTAAATTC ACGAGGAGGA CGCGTAAAAT CTGAAACCCA	8700
AACTGATATT GAAGGCATTA CCCGAATTAA ATATGAGATT CCTACACTAG ACAGGACAGG	8760
TAAACCTGAT GGTGGATTTA AGGAAATTTT AAGTATAAAA ACTGTTTATA ATCCTAAAAA	8820
ATTTTCTGAT GATAAAATAC TTCAAATGGC TCAAATGCT GCTTCACAAG GATATTCAAA	8880
AGCCTCTAAA ATTGCTCAAA ATGAAAGAAC TAAATCAATA TCGGAAAGAA AAAATGTCAT	8940
TCAATTCTCA GAAACCTTTG ACGGAATCAA ATTTAGATCA TATTTTGATG TAAATACAGG	9000
AAGAATTACA AACATTCACC CAGAATAATT TAAAGGAAAA ATTATGAAAA ATAATATTTT	9060
TCTAAACTTA AATAAAAAAT CTATAAATAA CAACCATTTT GTTATTTTGA TTTTTTTGA	9120
AACAATTTAC CAATTTGAAA CTAAAGATAC GCTTTTAGAG TGTTTTAAAA ATATTACAAC	9180
TACCGGACAT TTTGGAGTAA TAGGTGCTCA ATATGAAAA ATAGATGCTA CCAGATGGAT	9240
TGGAGATTAT GAAGAGGTAA ATGGATTTGA GTATATTGAT AAAGCTCCTT CTATTTATTT	9300
TTCAGTTGGA GATGATTTCA ATCCTGAAGA ATTAATTATA CCTATTAATT TAGCATATCA	9360

TTACTTTAAT ATTGCAATAT CTGATTTCTT AATAGCTCAC CCTGAATATC AAAAAAAGTG	9420
TAAAGAAATA CAAAAACAT ATTCTCAAAC AAAGTGTAGC CTGCATGAAA CCTAAAATCC	9480
ATGCGTAAGG TGTGTGCTTC AGCACGCACG CGTTCCATGA TTTACGGCTC AATGCCGTCT	9540
GAAAAGCTCA CAATTTTTCA GACGGCATTG GTTATGCAAG TAAATATTCA GATTCCCTAT	9600
ATACTGCCCA GACGCGTGCG TGCTGAAGAC ACCCCCTACG CTTGCTGCAG AACTTTTCGGG	9660
TAAAACCGGT GTGAGCATTG GCGCACCGTA TGCCAATGAG AACAGTCGCA TCCTGCTCAG	9720
CACCACGGAT ATCAGTTTCG AAAACGGCAA AATCAAAATT CAATCTTACG GTGACCAATA	9780
TTACTATGCG AGACAGAGCG AACTCTATAC CTTTGAACGC CGCAGCTACA AAACTGGCAA	9840
ATGGTACAAC CGCAAACACA TTACCGAAGT CAAAGAACAC AAAAACGCCA AGCCCGACGC	9900
AGTAAACCTC AGCGCATCCC AAGGCATCGA CATCAAATCT GGTGGCAGCA TCGACGCCTA	9960
CGCCACCGCA TTCGATGCCC CCAAAGGCAG CATTAAACATC GAAGCCGGGC GGAAATTGAC	10020
ACTCTATGCC GTAGAAGAGC TCAACTACGA CAACTAGAC AGCCAAAAAA GGCGCAGATT	10080
TCTCGGCATC AGCTACAGCA AAGCACACGA CACCACCACC CAAGTCATGA AAACCGCGCT	10140
GCCCTCAAGG GTAGTTGCAG AATCAGCCAA CCTCCAATCG GGCTGGGATA CCAAAGTGCA	10200
AGGCACACAG TTTGAAACCA CACTGGGTGG CGCAACCATA CGCGCAGGCG TAGGTGAGCA	10260
GGCACGGGCA GATGCCAAGA TTATCCTCGA AGGGATCAAA AGCAGCATCC ACACAGAAAC	10320
CGTGAGCAGC AGCAAATCTA CTCTATGGCA AAAACAGGCA GGACGGGGCA GTAACATCGA	10380
AACCTTGCAA TTGCCGAGTT TCACCGGTCC CGTTGCGCCC GTACTGTCCG CACCCGGCGG	10440

104T30 23482560

TTACATTGTC	GACATTCCGA	AAGGCAATCT	GAAAACCCAA	ATCGAAACCC	TCACCAAGCA	10500
GCCCCGAGTAT	GCTTATTTGA	AACAACTTCA	AGTTGCGAAA	AACATCAACT	GGAATCAGGT	10560
GCAGCTTGCT	TACGATAAAT	GGGACTACAA	ACAGGAGGGC	ATGACACCCG	CAGCAGCAGC	10620
TGTCGTCGTT	ATCGTCGTAA	CCGTATTGAC	CTACGGTGCA	CTGTCCGCCC	CGGCAGCCGC	10680
CGGAACGGCG	GGCGCGGCAG	GCGCAGGAGC	GGGAGGAGCC	GCAGCAGGAA	CGGCAGCCGG	10740
AACTGGAGTA	GCAGCAGGAA	CGGCAGCCAC	AACCGGAGTA	GCAGCAGGCA	CATCAGCTGC	10800
AGCTATCACC	ACAGCCGCAG	GCAAAGCCGC	ACTGGCCAGT	CTCGCCAGCC	AAGCCGCAGT	10860
TTCCCTCATC	AACAACAAAG	GAGACATAAA	CCATACCCTG	AAAGAACTGG	GCAAAAGCAG	10920
CACCGTCAGA	CAGGCCGCCA	CCGCCGCCGT	AACCGCAGGC	GTACTGCAGG	GCATAAGCGG	10980
GCTGAACACC	CAAGCAGCCG	AAGCCGTCAG	CAAACATTTT	CACAGTCCCG	CAGCAGGCAA	11040
ACTGACCGCT	AACCTGATCA	ACAGCACCGC	TGCCGCAAGT	GTCCATACCG	CCATCAACGG	11100
CGGCAGCCTG	AAAGACAAC	TGGGCGATGC	CGCACTGGGT	GCGATAGTCA	GTACCGTACA	11160
CGGAGAAGTA	GCGAGCAAAA	TCAAATTTAA	TCTCAGCGAA	GACTIONTTG	CCCACAAGAT	11220
AGCCCATGCC	GTAGCAGGCT	GTGCATCGGC	GGTAGCAAAT	AAAGGCAAAT	GTCGGGACGG	11280
CGCAATCGGC	GCGGCAGTCG	GCGAGATGGT	GGGAGAAACC	CTGTTGGACG	GACGCGATGT	11340
AGGCAAACTG	TCACCCCAAG	AACGCCAAAA	AGTCATAGCC	TACTCGCAGA	TTATCGCAGG	11400
CAGCGCAGTG	GCAATTGGTTA	AAGGGGATGT	GAATACGGCG	GTGAATGCGG	CTACTGTGGC	11460
AGTGGAGAAT	AATAGTCTTT	TAGCTCGCAG	GAGGGTAAAT	ATACGTTGGA	CTCCGCGACA	11520
AGAATTGGAA	CATGAATATG	CAATTCTTGA	AATCCAGGCC	ATTACCAATC	AAATCCGAAG	11580

GCTGGATCCG	AAATTTAACG	GGATTGCTAT	TCTGAGGACT	CCTGGAGAGC	CGTGGACAAG	11640
ACATGATGTA	CAAACATACA	GGCAATATTA	TAATCAATTA	AGGGAATCCA	GAGGCTTTGC	11700
TGTTGAACCA	ATTTATAGAA	TCAGGATAAA	CAACGGCAAT	GAATTTAACC	GTATCATGTC	11760
ATCAAAATAC	CCTTATAATG	AGCTTTATGT	AGCCAATCCT	AAATCGGCGA	CGGGGTATTT	11820
TAGGGTAGAT	TCGTATGATC	CTGCGACAAG	GGAAATTATT	TCAAGAAAAT	TTACCCAATT	11880
TTCTCAAATC	CAAGAAAGTA	CGGGGATTGG	TTATATCAAG	GAGGCTGTTA	GAAAATATAG	11940
CCCTGGTACT	GTCATTTCCA	ATGTTCCAAG	TACACCTACT	ACGATAAGAG	GAAGAAAAGCT	12000
TGAAGGAAAA	CTTATTTTAG	AAGTTCCTGC	TCAGGTCAAT	CCAATTCCAC	AATCTGTATT	12060
AAGGGCGGCA	CAAGAAGAAA	ATGTTATCAT	TAGAGATACA	ACAGGAAGGA	TTTACAAATG	12120
AAGAAAGATA	TTTTTTATTG	TGAGCAGTGG	TCTTATGGTT	ATAAGAGACT	TCATAAGCCT	12180
TTTTCTGAGA	AACAAGCTGA	GGAAAAACAT	CTTAAAGGGG	AGTTATATAC	TGCCGTAATA	12240
GGTTCGGCGA	CACAACCTGA	ATATGTAATT	ACCTTGCGAG	AGGAAGTAGG	TTTTTTTTTCG	12300
GTAAATTTTT	TCGATAAATT	TGGAAGGGAT	TATTTAACCC	ATCAATTTCA	AAAATATTCC	12360
AATTCGAATT	ATTATTTTCT	TTCTATGGCT	GTATGGAGAG	ATTATATAAC	TTTGAATCT	12420
CATGACTTAG	CAGAAGGATA	TACTTATTTT	TTCAATGAAA	ATACGGATGA	TTGCTATGTT	12480
TTGAAACAAG	ATTTTATTAA	TAATGAGCGA	TATGAAAAAA	CAGAATTATA	TTCCCAAAAA	12540
GATAAGGTAA	TTCTATTTCC	AAAGTTTGGT	GAATATGATT	TGGTGTTAAA	TCCGGACATT	12600
ATTTAATTAA	GTTTTAAGGC	CGTCTGAAAA	AAATTTCAAA	CGGCTTTTAT	TATTGGGTTT	12660

GGAATCTGAG GATAAAGCTG ATAAAAACCA GGAAATTATC AGATTGCTAT ATACGTATTG 12720  
 TTGTACAGAC TAAAGGCAGC AATCAAATCA CTATTGCTTA CCCACAAAAA TAAATTGATT 12780  
 ATATGGAATA ATCATGAATA AGAGAATGAA AATGTGTCCT GCTTGTCAAC AAGGCTATCT 12840  
 CTACCATTCTG AAACCTAAAT ATCTTCATGA TGAAATTATT CTGTGTGATG AATGCGATGC 12900  
 AGTATGGCTC AAAGGTATGA ATATATTTTA TGGAGAATAT GAAAAAGATT TTTATTCTTA 12960  
 TGTTCCTTTC ATGGAATCCC AAGGTATAAC GAGTGAATGT ATTTGGGAAG GAGATTGTGT 13020  
 TGATCATCCA TATTATGAAG ATGAAAACCTC AAATGATATG GATTGATGGA AATTTTAAGC 13080  
 CTGCGTAGGT ACGATTAGCC ATCAAACGGC GTAATCATAC GCAAGATTAT CAACAGAGAG 13140  
 GGCTGGCAGC GATATACCAC CCACAAGATT GCCCATGCCA TAGCGGGCTG TCGGCAGCG 13200  
 GCGGCGAATA AGGGCAAGTG TCAGGATGGT GCGATAGGCG CTGCAGTCGG TGAGATTGTT 13260  
 GGTGAGGCTT TGGTTAAGAA TACTGATTTT AGTCGTATGA GTGCGACCGA AATCGAAAAA 13320  
 GCTAAAGCGA AGATTACTGC CTATTCAAAA CTGGTTGCCG GCACTGCGTC TGCCGTTGTA 13380  
 GGCGGGGATG TGAATACAGC GGCGAATGCG GCACAGATAG CGGTGGAGAA TAATACTTTG 13440  
 TATCCTAGAT GCGTTGGTGC AAAGTGTGAT GAATTTCAAA AGGAACAACA AAAATGGATA 13500  
 CGTGAAAATC CTGAAGAATA TCGAGAAGTT TTGCTTTTTT AGACAGGATT TATTCCAATT 13560  
 ATCGGTGATA TACAGAGTTT TGTACAAGCA CAGACCGCTG CCGATCACCT GTTTGCTTTG 13620  
 CTGGGTGTGG TTCCGGGTAT CGGTGAATCG ATACAGGCCT ATAAAGTAGC GAAAGCGGCA 13680  
 AAAAATTTAC AAGGCATGAA AAAAGCCTTG GACAAGGCAG CAACCGTTGC CACTGCACAG 13740  
 GGCTATGTCA GCAAAACCAA AATCAAAATC GGTCAAACCTG AATTAAGGGT TACTGCAGCA 13800

0092045 004404  
 004404 0092045

ACTGACAAAC AATTGCTGAA AGCTATTGGC GAAGGAAGGG ACACGACAGG TAAAATGACC 13860  
 GAGCAGTTAT TTGACTCTTT AGCTAAACAA AATGGCTTCA GAGTGCTTTC GGGCGGCAAA 13920  
 TACGGCGGAA ATAACGGTTT TGATCATGTA TGGCAGGCTG CCGATGGTAG TGTCGTTTTG 13980  
 ATTGTAGAAA GTAAGCAGAT TAGGAACGGT ACGGTACAGC TGAATCCGAA TGGTGCGGGT 14040  
 GGATATACGC AAATGAGTGA GGATTGGATT AGACAAGTTT TAGATCAATT ACCCGATGGT 14100  
 AGTCCCGCTA AAGCTGCTGT CTTCAAAGCA AATAAGAACG GCACATTAAA AACAGCAATA 14160  
 GCAGGCGTTG ATCGTCAAAC AGGTAAGGCC GTTATTCTTC CTGTCAAAGT TCCTTCTAAA 14220  
 ACCAATATAA GGAGATAACA ATGGGGCACA ATATGATGAC CACCCAAAAA TGGTATGAGC 14280  
 ATATTACTAA TGTAATCATA GGCAATACTG CTAATTTCAA TAGCGGTTGC CTTGACTCTA 14340  
 TAGATTATGT AGATGAAAGA AAAGGCGTTC CGCTTGCAGC TATGCAACAT ATTTTCATGG 14400  
 ACGTTAGAGC TGCAGCTTCC CATGCCTATC TATTTGAACA TGATCTTAAG AAATTCAAGC 14460  
 AATATGCTTA TGTTGCAGGA AAGCTGGGGG TTTTGCTGAG TGTA AATTCT ACAGACCCTG 14520  
 AACCTTCTT CTTTCCCTGT GACATGCTCA ACATTCAAAA TCCGATGTTT CTGATGCTGA 14580  
 TGAGCGACAG CCCACAGCTG CGTGAGTTTC TGGTGCGCAA TATCGACAAC ATCGCCAACG 14640  
 ATACAGAAGC CTTTATAAAC CGCTACGACC TCAACCGGCA TATGATTTAC AATACTCTGC 14700  
 TGATGGTGA GGGTAAGCAG CTTGATCGGT TGAAACAACG TAGCGAGAAA GTCTTGCGGC 14760  
 ATCCCACCCC TAGCAAATGG CTGCAAAGC GGTGTACGA TTACCGCTTC TTCCTCGCTT 14820  
 TCGCCGAACA GGATGCCGAG GCAATGAAAG CCGCCTTAGA GCCGCTTTTC GATAAAAAA 14880

T04F0902E0660



CCGCGCGTAT GGCTGCCAAA GAAACATTGT CCTATTTCGA TTTCTACCTG CAGCCGCAAA 14940

TCGTTACCTA CGCCAAAATC GCATCCATGC ACGGTTTCGA TTTGGGCATA GATCAAGAAA 15000

TCTCACCGAG GGATTTGATT GTTTACGATC CGCTGCCGGC AGACGAATAT CAAGACATCT 15060

TCGATTTTAT GAAACAGTAT GACTTGTCTT ACCCGTATGA ATATCTGCAG GATTGGATAG 15120

ATTACTATAC GTTCAAAACC GATAAGCTGG TATTTGGTAA CGCGAAGCGA GAGTGAGCCG 15180

TAAAACTCTG AGCTCCTGTT TTATAGATTA CAACTTTAGG CCGTCTTAAA GCTGAAAGAT 15240

TTTCGAAAGC TATAAATTGA AGCCCTTCCA CAGTACATAG ATCTGTGTTG TGGCGGGGCT 15300

TTACCACGCT GATTGCCGGA GAAGAACTCA ACCTGCTGGC AAAACAAGGC ATGAGATCTT 15360

TGCAATAACA TGAGTTGAGA CCTTTGCAAA AAAGCCCTTC CCCGACATCC GAAACCCAAA 15420

CACAGGATTT CGGCTGTTTT CGTACCAAAT ACCTCCTAAT TTTACCCAAA TACCCCCTTA 15480

ATCCTCCTCG GACACCCGAT AATCAGGCAT CCGGGCTGCC TTTTAGGCGG CAGCGGGCGC 15540

ATTTAGCCTG TTGGCCGCTT TCAACAGGTT CAAACACATC GCCTTCAGGT GGCTTTGCGC 15600

ACTCACTTTG TCATTTCCAA 15620

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 acides aminés
- (B) TYPE : acide aminé
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: peptide

FBI/DOJ - 2025-04-24

(A) NAME/KEY: Protein  
(B) LOCATION:1..580

Met Lys Phe Phe Pro Ala Pro Cys Leu Leu Val Ile Leu Ala Val Ile  
1 5 10 15

Pro Leu Lys Thr Leu Ala Ala Asp Glu Asn Asp Ala Glu Leu Ile Arg  
20 25 30

Ser Met Gln Arg Gln Gln His Ile Asp Ala Glu Leu Leu Thr Asp Ala  
35 40 45

Asn Val Arg Phe Glu Gln Pro Leu Glu Lys Asn Asn Tyr Val Leu Ser  
50 55 60

Glu Asp Glu Thr Pro Cys Thr Arg Val Asn Tyr Ile Ser Leu Asp Asp  
65 70 75 80

Lys Thr Ala Arg Lys Phe Ser Phe Leu Pro Ser Val Leu Met Lys Glu  
85 90 95

Thr Ala Phe Lys Thr Gly Met Cys Leu Gly Ser Asn Asn Leu Ser Arg  
100 105 110

Leu Gln Lys Ala Ala Gln Gln Ile Leu Ile Val Arg Gly Tyr Leu Thr  
115 120 125

Ser Gln Ala Ile Ile Gln Pro Gln Asn Met Asp Ser Gly Ile Leu Lys  
130 135 140

Leu Arg Val Ser Ala Gly Glu Ile Gly Asp Ile Arg Tyr Glu Glu Lys  
145 150 155 160

Arg Asp Gly Lys Ser Ala Glu Gly Ser Ile Ser Ala Phe Asn Asn Lys

	165		170		175
Phe Pro Leu Tyr Arg Asn Lys Ile Leu Asn Leu Arg Asp Val Glu Gln					
	180		185		190
Gly Leu Glu Asn Leu Arg Arg Leu Pro Ser Val Lys Thr Asp Ile Gln					
	195		200		205
Ile Ile Pro Ser Glu Glu Glu Gly Lys Ser Asp Leu Gln Ile Lys Trp					
	210		215		220
Gln Gln Asn Lys Pro Ile Arg Phe Ser Ile Gly Ile Asp Asp Ala Gly					
	225		230		235 240
Gly Lys Thr Thr Gly Lys Tyr Gln Gly Asn Val Ala Leu Ser Phe Asp					
	245		250		255
Asn Pro Leu Gly Leu Ser Asp Leu Phe Tyr Val Ser Tyr Gly Arg Gly					
	260		265		270
Leu Val His Lys Thr Asp Leu Thr Asp Ala Thr Gly Thr Glu Thr Glu					
	275		280		285
Ser Gly Ser Arg Ser Tyr Ser Val His Tyr Ser Val Pro Val Lys Lys					
	290		295		300
Trp Leu Phe Ser Phe Asn His Asn Gly His Arg Tyr His Glu Ala Thr					
	305		310		315 320
Glu Gly Tyr Ser Val Asn Tyr Asp Tyr Asn Gly Lys Gln Tyr Gln Ser					
	325		330		335
Ser Leu Ala Ala Glu Arg Met Leu Trp Arg Asn Arg Phe His Lys Thr					
	340		345		350
Ser Val Gly Met Lys Leu Trp Thr Arg Gln Thr Tyr Lys Tyr Ile Asp					

104733" 2542660

355																			
Asp	Ala	Glu	Ile	Glu	Val	Gln	Arg	Arg	Arg	Ser	Ala	Gly	Trp	Glu	Ala				
370						375						380							
Glu	Leu	Arg	His	Arg	Ala	Tyr	Leu	Asn	Arg	Trp	Gln	Leu	Asp	Gly	Lys				
385					390					395					400				
Leu	Ser	Tyr	Lys	Arg	Gly	Thr	Gly	Met	Arg	Gln	Ser	Met	Pro	Ala	Pro				
				405					410					415					
Glu	Glu	Asn	Gly	Gly	Gly	Thr	Ile	Pro	Gly	Thr	Ser	Arg	Met	Lys	Ile				
			420					425					430						
Ile	Thr	Ala	Gly	Leu	Asp	Ala	Ala	Ala	Pro	Phe	Met	Leu	Gly	Lys	Gln				
		435					440					445							
Gln	Phe	Phe	Tyr	Ala	Thr	Ala	Ile	Gln	Ala	Gln	Trp	Asn	Lys	Thr	Pro				
450						455					460								
Leu	Val	Ala	Gln	Asp	Lys	Leu	Ser	Ile	Gly	Ser	Arg	Tyr	Thr	Val	Arg				
465					470					475					480				
Gly	Phe	Asp	Gly	Glu	Gln	Ser	Leu	Phe	Gly	Glu	Arg	Gly	Phe	Tyr	Trp				
			485						490					495					
Gln	Asn	Thr	Leu	Thr	Trp	Tyr	Phe	His	Pro	Asn	His	Gln	Phe	Tyr	Leu				
		500						505					510						
Gly	Ala	Asp	Tyr	Gly	Arg	Val	Ser	Gly	Glu	Ser	Ala	Gln	Tyr	Val	Ser				
	515						520					525							
Gly	Lys	Gln	Leu	Met	Gly	Ala	Val	Val	Gly	Phe	Arg	Gly	Gly	His	Lys				
530						535						540							
Val	Gly	Gly	Met	Phe	Ala	Tyr	Asp	Leu	Phe	Ala	Gly	Lys	Pro	Leu	His				
545					550						555				560				

Asn Tyr Ser Phe  
580

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1981 acides aminés  
(B) TYPE : acide aminé  
(C) STRANDEDNESS: single  
(D) TOPOLOGY : linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide  
(B) LOCATION:1..1981

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Met Asn Lys Gly Leu His Arg Ile Ile Phe Ser Lys Lys His Ser Thr  
1 5 10 15

Met Val Ala Val Ala Glu Thr Ala Asn Ser Gln Gly Lys Gly Lys Gln  
20 25 30

Ala Gly Ser Ser Val Ser Val Ser Leu Lys Thr Ser Gly Asp Leu Cys  
35 40 45

Gly Lys Leu Lys Thr Thr Leu Lys Thr Leu Val Cys Ser Leu Val Ser  
50 55 60

Leu Ser Met Val Leu Pro Ala His Ala Gln Ile Thr Thr Asp Lys Ser

65		70		75		80									
Ala	Pro	Lys	Asn	Gln	Gln	Val	Val	Ile	Leu	Lys	Thr	Asn	Thr	Gly	Ala
				85					90					95	
Pro	Leu	Val	Asn	Ile	Gln	Thr	Pro	Asn	Gly	Arg	Gly	Leu	Ser	His	Asn
			100					105					110		
Arg	Tyr	Thr	Gln	Phe	Asp	Val	Asp	Asn	Lys	Gly	Ala	Val	Leu	Asn	Asn
		115					120						125		
Asp	Arg	Asn	Asn	Asn	Pro	Phe	Leu	Val	Lys	Gly	Ser	Ala	Gln	Leu	Ile
		130				135						140			
Leu	Asn	Glu	Val	Arg	Gly	Thr	Ala	Ser	Lys	Leu	Asn	Gly	Ile	Val	Thr
145					150					155				160	
Val	Gly	Gly	Gln	Lys	Ala	Asp	Val	Ile	Ile	Ala	Asn	Pro	Asn	Gly	Ile
			165						170					175	
Thr	Val	Asn	Gly	Gly	Gly	Phe	Lys	Asn	Val	Gly	Arg	Gly	Ile	Leu	Thr
			180					185						190	
Ile	Gly	Ala	Pro	Gln	Ile	Gly	Lys	Asp	Gly	Ala	Leu	Thr	Gly	Phe	Asp
		195					200						205		
Val	Arg	Gln	Gly	Thr	Leu	Thr	Val	Gly	Ala	Ala	Gly	Trp	Asn	Asp	Lys
		210					215					220			
Gly	Gly	Ala	Asp	Tyr	Thr	Gly	Val	Leu	Ala	Arg	Ala	Val	Ala	Leu	Gln
225					230					235				240	
Gly	Lys	Leu	Gln	Gly	Lys	Asn	Leu	Ala	Val	Ser	Thr	Gly	Pro	Gln	Lys
			245						250					255	
Val	Asp	Tyr	Ala	Ser	Gly	Glu	Ile	Ser	Ala	Gly	Thr	Ala	Ala	Gly	Thr
			260						265					270	

F04T33 45423660

Lys Pro Thr Ile Ala Leu Asp Thr Ala Ala Leu Gly Gly Met Tyr Ala  
 275 280 285

Asp Ser Ile Thr Leu Ile Ala Asn Glu Lys Gly Val Gly Val Lys Asn  
 290 295 300

Ala Gly Thr Leu Glu Ala Ala Lys Gln Leu Ile Val Thr Ser Ser Gly  
 305 310 315 320

Arg Ile Glu Asn Ser Gly Arg Ile Ala Thr Thr Ala Asp Gly Thr Glu  
 325 330 335

Ala Ser Pro Thr Tyr Leu Ser Ile Glu Thr Thr Glu Lys Gly Ala Ala  
 340 345 350

Gly Thr Phe Ile Ser Asn Gly Gly Arg Ile Glu Ser Lys Gly Leu Leu  
 355 360 365

Val Ile Glu Thr Gly Glu Asp Ile Ser Leu Arg Asn Gly Ala Val Val  
 370 375 380

Gln Asn Asn Gly Ser Arg Pro Ala Thr Thr Val Leu Asn Ala Gly His  
 385 390 395 400

Asn Leu Val Ile Glu Ser Lys Thr Asn Val Asn Asn Ala Lys Gly Ser  
 405 410 415

Ala Asn Leu Ser Ala Gly Gly Arg Thr Thr Ile Asn Asp Ala Thr Ile  
 420 425 430

Gln Ala Gly Ser Ser Val Tyr Ser Ser Thr Lys Gly Asp Thr Glu Leu  
 435 440 445

Gly Glu Asn Thr Arg Ile Ile Ala Glu Asn Val Thr Val Leu Ser Asn  
 450 455 460

104133 254650

Gly Ser Ile Gly Ser Ala Ala Val Ile Glu Ala Lys Asp Thr Ala His  
465 470 475 480

Ile Glu Ser Gly Lys Pro Leu Ser Leu Glu Thr Ser Thr Val Ala Ser  
485 490 495

Asn Ile Arg Leu Asn Asn Gly Asn Ile Lys Gly Gly Lys Gln Leu Ala  
500 505 510

Leu Leu Ala Asp Asp Asn Ile Thr Ala Lys Thr Thr Asn Leu Asn Thr  
515 520 525

Pro Gly Asn Leu Tyr Val His Thr Gly Lys Asp Leu Asn Leu Asn Val  
530 535 540

Asp Lys Asp Leu Ser Ala Ala Ser Ile His Leu Lys Ser Asp Asn Ala  
545 550 555 560

Ala His Ile Thr Gly Thr Ser Lys Thr Leu Thr Ala Ser Lys Asp Met  
565 570 575

Gly Val Glu Ala Gly Leu Leu Asn Val Thr Asn Thr Asn Leu Arg Thr  
580 585 590

Asn Ser Gly Asn Leu His Ile Gln Ala Ala Lys Gly Asn Ile Gln Leu  
595 600 605

Arg Asn Thr Lys Leu Asn Ala Ala Lys Ala Leu Glu Thr Thr Ala Leu  
610 615 620

Gln Gly Asn Ile Val Ser Asp Gly Leu His Ala Val Ser Ala Asp Gly  
625 630 635 640

His Val Ser Leu Leu Ala Asn Gly Asn Ala Asp Phe Thr Gly His Asn  
645 650 655

Thr Leu Thr Ala Lys Ala Asp Val Asn Ala Gly Ser Val Gly Lys Gly

104700 234660



660	665	670
Arg Leu Lys Ala Asp Asn Thr Asn Ile Thr Ser Ser Ser Gly Asp Ile		
675	680	685
Thr Leu Val Ala Gly Asn Gly Ile Gln Leu Gly Asp Gly Lys Gln Arg		
690	695	700
Asn Ser Ile Asn Gly Lys His Ile Ser Ile Lys Asn Asn Gly Gly Asn		
705	710	715 720
Ala Asp Leu Lys Asn Leu Asn Val His Ala Lys Ser Gly Ala Leu Asn		
725	730	735
Ile His Ser Asp Arg Ala Leu Ser Ile Glu Asn Thr Lys Leu Glu Ser		
740	745	750
Thr His Asn Thr His Leu Asn Ala Gln His Glu Arg Val Thr Leu Asn		
755	760	765
Gln Val Asp Ala Tyr Ala His Arg His Leu Ser Ile Thr Gly Ser Gln		
770	775	780
Ile Trp Gln Asn Asp Lys Leu Pro Ser Ala Asn Lys Leu Val Ala Asn		
785	790	795 800
Gly Val Leu Ala Leu Asn Ala Arg Tyr Ser Gln Ile Ala Asp Asn Thr		
805	810	815
Thr Leu Arg Ala Gly Ala Ile Asn Leu Thr Ala Gly Thr Ala Leu Val		
820	825	830
Lys Arg Gly Asn Ile Asn Trp Ser Thr Val Ser Thr Lys Thr Leu Glu		
835	840	845
Asp Asn Ala Glu Leu Lys Pro Leu Ala Gly Arg Leu Asn Ile Glu Ala		
850	855	860

04730 2540663

Gly Ser Gly Thr Leu Thr Ile Glu Pro Ala Asn Arg Ile Ser Ala His  
865 870 875 880

Thr Asp Leu Ser Ile Lys Thr Gly Gly Lys Leu Leu Leu Ser Ala Lys  
885 890 895

Gly Gly Asn Ala Gly Ala Pro Ser Ala Gln Val Ser Ser Leu Glu Ala  
900 905 910

Lys Gly Asn Ile Arg Leu Val Thr Gly Glu Thr Asp Leu Arg Gly Ser  
915 920 925

Lys Ile Thr Ala Gly Lys Asn Leu Val Val Ala Thr Thr Lys Gly Lys  
930 935 940

Leu Asn Ile Glu Ala Val Asn Asn Ser Phe Ser Asn Tyr Phe Pro Thr  
945 950 955 960

Gln Lys Ala Ala Glu Leu Asn Gln Lys Ser Lys Glu Leu Glu Gln Gln  
965 970 975

Ile Ala Gln Leu Lys Lys Ser Ser Pro Lys Ser Lys Leu Ile Pro Thr  
980 985 990

Leu Gln Glu Glu Arg Asp Arg Leu Ala Phe Tyr Ile Gln Ala Ile Asn  
995 1000 1005

Lys Glu Val Lys Gly Lys Lys Pro Lys Gly Lys Glu Tyr Leu Gln Ala  
1010 1015 1020

Lys Leu Ser Ala Gln Asn Ile Asp Leu Ile Ser Ala Gln Gly Ile Glu  
1025 1030 1035 1040

Ile Ser Gly Ser Asp Ile Thr Ala Ser Lys Lys Leu Asn Leu His Ala  
1045 1050 1055

1044 99 4343660

Ala Gly Val Leu Pro Lys Ala Ala Asp Ser Glu Ala Ala Ala Ile Leu  
 1060 1065 1070

Ile Asp Gly Ile Thr Asp Gln Tyr Glu Ile Gly Lys Pro Thr Tyr Lys  
 1075 1080 1085

Ser His Tyr Asp Lys Ala Ala Leu Asn Lys Pro Ser Arg Leu Thr Gly  
 1090 1095 1100

Arg Thr Gly Val Ser Ile His Ala Ala Ala Ala Leu Asp Asp Ala Arg  
 1105 1110 1115 1120

Ile Ile Ile Gly Ala Ser Glu Ile Lys Ala Pro Ser Gly Ser Ile Asp  
 1125 1130 1135

Ile Lys Ala His Ser Asp Ile Val Leu Glu Ala Gly Gln Asn Asp Ala  
 1140 1145 1150

Tyr Thr Phe Leu Lys Thr Lys Gly Lys Ser Gly Lys Ile Ile Arg Lys  
 1155 1160 1165

Thr Lys Phe Thr Ser Thr Arg Asp His Leu Ile Met Pro Ala Pro Val  
 1170 1175 1180

Glu Leu Thr Ala Asn Gly Ile Thr Leu Gln Ala Gly Gly Asn Ile Glu  
 1185 1190 1195 1200

Ala Asn Thr Thr Arg Phe Asn Ala Pro Ala Gly Lys Val Thr Leu Val  
 1205 1210 1215

Ala Gly Glu Glu Leu Gln Leu Leu Ala Glu Glu Gly Ile His Lys His  
 1220 1225 1230

Glu Leu Asp Val Gln Lys Ser Arg Arg Phe Ile Gly Ile Lys Val Gly  
 1235 1240 1245

1060 1065 1070 1075 1080 1085 1090 1095 1100 1105 1110 1115 1120 1125 1130 1135 1140 1145 1150 1155 1160 1165 1170 1175 1180 1185 1190 1195 1200 1205 1210 1215 1220 1225 1230 1235 1240 1245

Lys Ser Asn Tyr Ser Lys Asn Glu Leu Asn Glu Thr Lys Leu Pro Val  
 1250 1255 1260

Arg Val Val Ala Gln Thr Ala Ala Thr Arg Ser Gly Trp Asp Thr Val  
 1265 1270 1275 1280

Leu Glu Gly Thr Glu Phe Lys Thr Thr Leu Ala Gly Ala Asp Ile Gln  
 1285 1290 1295

Ala Gly Val Gly Glu Lys Ala Arg Val Asp Ala Lys Ile Ile Leu Lys  
 1300 1305 1310

Gly Ile Val Asn Arg Ile Gln Ser Glu Glu Lys Leu Glu Thr Asn Ser  
 1315 1320 1325

Thr Val Trp Gln Lys Gln Ala Gly Arg Gly Ser Thr Ile Glu Thr Leu  
 1330 1335 1340

Lys Leu Pro Ser Phe Glu Ser Pro Thr Pro Pro Lys Leu Ser Ala Pro  
 1345 1350 1355 1360

Gly Gly Tyr Ile Val Asp Ile Pro Lys Gly Asn Leu Lys Thr Glu Ile  
 1365 1370 1375

Glu Lys Leu Ser Lys Gln Pro Glu Tyr Ala Tyr Leu Lys Gln Leu Gln  
 1380 1385 1390

Val Ala Lys Asn Ile Asn Trp Asn Gln Val Gln Leu Ala Tyr Asp Arg  
 1395 1400 1405

Trp Asp Tyr Lys Gln Glu Gly Leu Thr Glu Ala Gly Ala Ala Ile Ile  
 1410 1415 1420

Ala Leu Ala Val Thr Val Val Thr Ser Gly Ala Gly Thr Gly Ala Val  
 1425 1430 1435 1440

1250 1255 1260 1265 1270 1275 1280 1285 1290 1295 1300 1305 1310 1315 1320 1325 1330 1335 1340 1345 1350 1355 1360 1365 1370 1375 1380 1385 1390 1395 1400 1405 1410 1415 1420 1425 1430 1435 1440

Leu Gly Leu Asn Gly Ala Ala Ala Thr Asp Ala Ala Phe Ala	1445	1450	1455
Ser Leu Ala Ser Gln Ala Ser Val Ser Phe Ile Asn Asn Lys Gly Asp	1460	1465	1470
Val Gly Lys Thr Leu Lys Glu Leu Gly Arg Ser Ser Thr Val Lys Asn	1475	1480	1485
Leu Val Val Ala Ala Ala Thr Ala Gly Val Ala Asp Lys Ile Gly Ala	1490	1495	1500
Ser Ala Leu Asn Asn Val Ser Asp Lys Gln Trp Ile Asn Asn Leu Thr	1505	1510	1520
Val Asn Leu Ala Asn Ala Gly Ser Ala Ala Leu Ile Asn Thr Ala Val	1525	1530	1535
Asn Gly Gly Ser Leu Lys Asp Asn Leu Glu Ala Asn Ile Leu Ala Ala	1540	1545	1550
Leu Val Asn Thr Ala His Gly Glu Ala Ala Ser Lys Ile Lys Gln Leu	1555	1560	1565
Asp Gln His Tyr Ile Val His Lys Ile Ala His Ala Ile Ala Gly Cys	1570	1575	1580
Ala Ala Ala Ala Ala Asn Lys Gly Lys Cys Gln Asp Gly Ala Ile Gly	1585	1590	1600
Ala Ala Val Gly Glu Ile Val Gly Glu Ala Leu Thr Asn Gly Lys Asn	1605	1610	1615
Pro Asp Thr Leu Thr Ala Lys Glu Arg Glu Gln Ile Leu Ala Tyr Ser	1620	1625	1630
Lys Leu Val Ala Gly Thr Val Ser Gly Val Val Gly Gly Asp Val Asn			

1635	1640	1645
Ala Ala Ala Asn Ala Ala Glu Val Ala Val Lys Asn Asn Gln Leu Ser		
1650	1655	1660
Asp Lys Glu Gly Arg Glu Phe Asp Asn Glu Met Thr Ala Cys Ala Lys		
1665	1670	1675 1680
Gln Asn Asn Pro Gln Leu Cys Arg Lys Asn Thr Val Lys Lys Tyr Gln		
1685	1690	1695
Asn Val Ala Asp Lys Arg Leu Ala Ala Ser Ile Ala Ile Cys Thr Asp		
1700	1705	1710
Ile Ser Arg Ser Thr Glu Cys Arg Thr Ile Arg Lys Gln His Leu Ile		
1715	1720	1725
Asp Ser Arg Ser Leu His Ser Ser Trp Glu Ala Gly Leu Ile Gly Lys		
1730	1735	1740
Asp Asp Glu Trp Tyr Lys Leu Phe Ser Lys Ser Tyr Thr Gln Ala Asp		
1745	1750	1755 1760
Leu Ala Leu Gln Ser Tyr His Leu Asn Thr Ala Ala Lys Ser Trp Leu		
1765	1770	1775
Gln Ser Gly Asn Thr Lys Pro Leu Ser Glu Trp Met Ser Asp Gln Gly		
1780	1785	1790
Tyr Thr Leu Ile Ser Gly Val Asn Pro Arg Phe Ile Pro Ile Pro Arg		
1795	1800	1805
Gly Phe Val Lys Gln Asn Thr Pro Ile Thr Asn Val Lys Tyr Pro Glu		
1810	1815	1820
Gly Ile Ser Phe Asp Thr Asn Leu Lys Arg His Leu Ala Asn Ala Asp		
1825	1830	1835 1840

F04T32 25423663

Gly Phe Ser Gln Glu Gln Gly Ile Lys Gly Ala His Asn Arg Thr Asn  
 1845 1850 1855

Phe Met Ala Glu Leu Asn Ser Arg Gly Gly Arg Val Lys Ser Glu Thr  
 1860 1865 1870

Gln Thr Asp Ile Glu Gly Ile Thr Arg Ile Lys Tyr Glu Ile Pro Thr  
 1875 1880 1885

Leu Asp Arg Thr Gly Lys Pro Asp Gly Gly Phe Lys Glu Ile Ser Ser  
 1890 1895 1900

Ile Lys Thr Val Tyr Asn Pro Lys Lys Phe Ser Asp Asp Lys Ile Leu  
 1905 1910 1915 1920

Gln Met Ala Gln Asn Ala Ala Ser Gln Gly Tyr Ser Lys Ala Ser Lys  
 1925 1930 1935

Ile Ala Gln Asn Glu Arg Thr Lys Ser Ile Ser Glu Arg Lys Asn Val  
 1940 1945 1950

Ile Gln Phe Ser Glu Thr Phe Asp Gly Ile Lys Phe Arg Ser Tyr Phe  
 1955 1960 1965

Asp Val Asn Thr Gly Arg Ile Thr Asn Ile His Pro Glu  
 1970 1975 1980

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 acides aminés
- (B) TYPE : acide aminé
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

F04T30/234B2660

(ix) **FEATURE:**

(B) LOCATION:1..143

Met Lys Asn Asn Ile Phe Leu Asn Leu Asn Lys Lys Ser Ile Asn Asn  
1 5 10 15

Asn His Phe Val Ile Ser Ile Phe Phe Glu Thr Ile Tyr Gln Phe Glu  
20 25 30

Thr Lys Asp Thr Leu Leu Glu Cys Phe Lys Asn Ile Thr Thr Thr Gly  
35 40 45

His Phe Gly Val Ile Gly Ala Gln Tyr Glu Lys Ile Asp Ala Thr Arg  
50 55 60

Trp Ile Gly Asp Tyr Glu Glu Val Asn Gly Phe Glu Tyr Ile Asp Lys  
65                      70                      75                      80

Ala Pro Ser Ile Tyr Phe Ser Val Gly Asp Asp Phe Asn Pro Glu Glu  
85 90 95

Leu Ile Ile Pro Ile Asn Leu Ala Tyr His Tyr Phe Asn Ile Ala Ile  
100 105 110

Ser Asp Phe Leu Ile Ala His Pro Glu Tyr Gln Lys Lys Cys Lys Glu  
115 120 125

Ile Gln Lys Thr Tyr Ser Gln Thr Asn Cys Ser Leu His Glu Thr  
130 135 140



## (2) INFORMATION FOR SEQ ID NO: 40:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 acides aminés
- (B) TYPE : acide aminé
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION:1..833

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

Val Leu Lys Thr Pro Pro Thr Leu Ala Ala Glu Leu Ser Gly Lys Thr  
1 5 10 15

Gly Val Ser Ile Ser Ala Pro Tyr Ala Asn Glu Asn Ser Arg Ile Leu  
20 25 30

Leu Ser Thr Thr Asp Ile Ser Ser Glu Asn Gly Lys Ile Lys Ile Gln  
35 40 45

Ser Tyr Gly Asp Gln Tyr Tyr Tyr Ala Arg Gln Ser Glu Leu Tyr Thr  
50 55 60

Phe Glu Arg Arg Ser Tyr Lys Thr Gly Lys Trp Tyr Asn Arg Lys His  
65 70 75 80

Ile Thr Glu Val Lys Glu His Lys Asn Ala Lys Pro Asp Ala Val Asn  
85 90 95

Leu Ser Ala Ser Gln Gly Ile Asp Ile Lys Ser Gly Gly Ser Ile Asp  
100 105 110

F04T80 2342660

Ala Tyr Ala Thr Ala Phe Asp Ala Pro Lys Gly Ser Ile Asn Ile Glu  
115 120 125

Ala Gly Arg Lys Leu Thr Leu Tyr Ala Val Glu Glu Leu Asn Tyr Asp  
130 135 140

Lys Leu Asp Ser Gln Lys Arg Arg Arg Phe Leu Gly Ile Ser Tyr Ser  
145 150 155 160

Lys Ala His Asp Thr Thr Thr Gln Val Met Lys Thr Ala Leu Pro Ser  
165 170 175

Arg Val Val Ala Glu Ser Ala Asn Leu Gln Ser Gly Trp Asp Thr Lys  
180 185 190

Leu Gln Gly Thr Gln Phe Glu Thr Thr Leu Gly Gly Ala Thr Ile Arg  
195 200 205

Ala Gly Val Gly Glu Gln Ala Arg Ala Asp Ala Lys Ile Ile Leu Glu  
210 215 220

Gly Ile Lys Ser Ser Ile His Thr Glu Thr Val Ser Ser Ser Lys Ser  
225 230 235 240

Thr Leu Trp Gln Lys Gln Ala Gly Arg Gly Ser Asn Ile Glu Thr Leu  
245 250 255

Gln Leu Pro Ser Phe Thr Gly Pro Val Ala Pro Val Leu Ser Ala Pro  
260 265 270

Gly Gly Tyr Ile Val Asp Ile Pro Lys Gly Asn Leu Lys Thr Gln Ile  
275 280 285

Glu Thr Leu Thr Lys Gln Pro Glu Tyr Ala Tyr Leu Lys Gln Leu Gln  
290 295 300

FOOTNOTES 4542660

Asn Ser Thr Ala Ala Ala Ser Val His Thr Ala Ile Asn Gly Gly Ser  
485 490 495

Leu	Lys	Asp	Asn	Leu	Gly	Asp	Ala	Ala	Leu	Gly	Ala	Ile	Val	Ser	Thr	
			500						505					510		
Val	His	Gly	Glu	Val	Ala	Ser	Lys	Ile	Lys	Phe	Asn	Leu	Ser	Glu	Asp	
		515					520					525				
Tyr	Ile	Ala	His	Lys	Ile	Ala	His	Ala	Val	Ala	Gly	Cys	Ala	Ser	Ala	
	530					535					540					
Val	Ala	Asn	Lys	Gly	Lys	Cys	Arg	Asp	Gly	Ala	Ile	Gly	Ala	Ala	Val	
545					550					555					560	
Gly	Glu	Met	Val	Gly	Glu	Thr	Leu	Leu	Asp	Gly	Arg	Asp	Val	Gly	Lys	
				565					570					575		
Leu	Ser	Pro	Gln	Glu	Arg	Gln	Lys	Val	Ile	Ala	Tyr	Ser	Gln	Ile	Ile	
			580					585					590			
Ala	Gly	Ser	Ala	Val	Ala	Leu	Val	Lys	Gly	Asp	Val	Asn	Thr	Ala	Val	
		595					600					605				
Asn	Ala	Ala	Thr	Val	Ala	Val	Glu	Asn	Asn	Ser	Leu	Leu	Ala	Arg	Arg	
	610					615						620				
Arg	Val	Asn	Ile	Arg	Trp	Thr	Pro	Arg	Gln	Glu	Leu	Glu	His	Glu	Tyr	
625					630					635					640	
Ala	Ile	Leu	Glu	Ile	Gln	Ala	Ile	Thr	Asn	Gln	Ile	Arg	Arg	Leu	Asp	
				645					650					655		
Pro	Lys	Phe	Asn	Gly	Ile	Ala	Ile	Leu	Arg	Thr	Pro	Gly	Glu	Pro	Trp	
			660					665					670			
Thr	Arg	His	Asp	Val	Gln	Thr	Tyr	Arg	Gln	Tyr	Tyr	Asn	Gln	Leu	Arg	
		675						680					685			

Glu Ser Arg Gly Phe Ala Val Glu Pro Ile Tyr Arg Ile Arg Ile Asn  
 690 695 700

Asn Gly Asn Glu Phe Asn Arg Ile Met Ser Ser Lys Tyr Pro Tyr Asn  
 705 710 715 720

Glu Leu Tyr Val Ala Asn Pro Lys Ser Ala Thr Gly Tyr Phe Arg Val  
 725 730 735

Asp Ser Tyr Asp Pro Ala Thr Arg Glu Ile Ile Ser Arg Lys Phe Thr  
 740 745 750

Gln Phe Ser Gln Ile Gln Glu Ser Thr Gly Ile Gly Tyr Ile Lys Glu  
 755 760 765

Ala Val Arg Lys Tyr Ser Pro Gly Thr Val Ile Ser Asn Val Pro Ser  
 770 775 780

Thr Pro Thr Thr Ile Arg Gly Arg Lys Leu Glu Gly Lys Leu Ile Leu  
 785 790 795 800

Glu Val Pro Ala Gln Val Asn Pro Ile Pro Gln Ser Val Leu Arg Ala  
 805 810 815

Ala Gln Glu Glu Asn Val Ile Ile Arg Asp Thr Thr Gly Arg Ile Tyr  
 820 825 830

Lys

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 664 acides aminés
- (B) TYPE : acide aminé
- (D) TOPOLOGY : linear

FOR "JEBE" 2412660

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

									Met	Lys	Thr	Ala	Leu	Pro	Ser		
									170							175	
Arg	Val	Val	Ala	Glu	Ser	Ala	Asn	Leu	Gln	Ser	Gly	Trp	Asp	Thr	Lys		
			180					185					190				
Leu	Gln	Gly	Thr	Gln	Phe	Glu	Thr	Thr	Leu	Gly	Gly	Ala	Thr	Ile	Arg		
		195					200					205					
Ala	Gly	Val	Gly	Glu	Gln	Ala	Arg	Ala	Asp	Ala	Lys	Ile	Ile	Leu	Glu		
	210					215					220						
Gly	Ile	Lys	Ser	Ser	Ile	His	Thr	Glu	Thr	Val	Ser	Ser	Ser	Lys	Ser		
225					230					235					240		
Thr	Leu	Trp	Gln	Lys	Gln	Ala	Gly	Arg	Gly	Ser	Asn	Ile	Glu	Thr	Leu		
			245					250					255				
Gln	Leu	Pro	Ser	Phe	Thr	Gly	Pro	Val	Ala	Pro	Val	Leu	Ser	Ala	Pro		
		260					265					270					
Gly	Gly	Tyr	Ile	Val	Asp	Ile	Pro	Lys	Gly	Asn	Leu	Lys	Thr	Gln	Ile		
	275					280					285						
Glu	Thr	Leu	Thr	Lys	Gln	Pro	Glu	Tyr	Ala	Tyr	Leu	Lys	Gln	Leu	Gln		
290					295					300							
Val	Ala	Lys	Asn	Ile	Asn	Trp	Asn	Gln	Val	Gln	Leu	Ala	Tyr	Asp	Lys		
305			310					315						320			
Trp	Asp	Tyr	Lys	Gln	Glu	Gly	Met	Thr	Pro	Ala	Ala	Ala	Ala	Val	Val		
			325					330						335			
Val	Ile	Val	Val	Thr	Val	Leu	Thr	Tyr	Gly	Ala	Leu	Ser	Ala	Pro	Ala		
	340					345					350						

Tyr Ile Ala His Lys Ile Ala His Ala Val Ala Gly Cys Ala Ser Ala  
530 535 540

Val Ala Asn Lys Gly Lys Cys Arg Asp Gly Ala Ile Gly Ala Ala Val  
545 550 555 560

Gly Glu Met Val Gly Glu Thr Leu Leu Asp Gly Arg Asp Val Gly Lys  
565 570 575

Leu Ser Pro Gln Glu Arg Gln Lys Val Ile Ala Tyr Ser Gln Ile Ile  
580 585 590

Ala Gly Ser Ala Val Ala Leu Val Lys Gly Asp Val Asn Thr Ala Val  
595 600 605

Asn Ala Ala Thr Val Ala Val Glu Asn Asn Ser Leu Leu Ala Arg Arg  
610 615 620

Arg Val Asn Ile Arg Trp Thr Pro Arg Gln Glu Leu Glu His Glu Tyr  
625 630 635 640

Ala Ile Leu Glu Ile Gln Ala Ile Thr Asn Gln Ile Arg Arg Leu Asp  
645 650 655

Pro Lys Phe Asn Gly Ile Ala Ile Leu Arg Thr Pro Gly Glu Pro Trp  
660 665 670

Thr Arg His Asp Val Gln Thr Tyr Arg Gln Tyr Tyr Asn Gln Leu Arg  
675 680 685

Glu Ser Arg Gly Phe Ala Val Glu Pro Ile Tyr Arg Ile Arg Ile Asn  
690 695 700

Asn Gly Asn Glu Phe Asn Arg Ile Met Ser Ser Lys Tyr Pro Tyr Asn  
705 710 715 720

Glu Leu Tyr Val Ala Asn Pro Lys Ser Ala Thr Gly Tyr Phe Arg Val  
725 730 735

FOOTNOTES 4242660



Asp Ser Tyr Asp Pro Ala Thr Arg Glu Ile Ile Ser Arg Lys Phe Thr  
 740 745 750

Gln Phe Ser Gln Ile Gln Glu Ser Thr Gly Ile Gly Tyr Ile Lys Glu  
 755 760 765

Ala Val Arg Lys Tyr Ser Pro Gly Thr Val Ile Ser Asn Val Pro Ser  
 770 775 780

Thr Pro Thr Thr Ile Arg Gly Arg Lys Leu Glu Gly Lys Leu Ile Leu  
 785 790 795 800

Glu Val Pro Ala Gln Val Asn Pro Ile Pro Gln Ser Val Leu Arg Ala  
 805 810 815

Ala Gln Glu Glu Asn Val Ile Ile Arg Asp Thr Thr Gly Arg Ile Tyr  
 820 825 830

Lys

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 acides aminés
- (B) TYPE : acide aminé
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION:1..162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

Met Lys Lys Asp Ile Phe Tyr Cys Glu Gln Trp Ser Tyr Gly Tyr Lys  
 1 5 10 15

F04F03A01

Arg Leu His Lys Pro Phe Ser Glu Lys Gln Ala Glu Glu Lys His Leu  
20 25 30

Lys Gly Glu Leu Tyr Thr Ala Val Ile Gly Ser Ala Thr Gln Pro Glu  
35 40 45

Tyr Val Ile Thr Leu Arg Glu Glu Val Gly Phe Phe Ser Val Asn Phe  
50 55 60

Phe Asp Lys Phe Gly Arg Asp Tyr Leu Thr His Gln Phe Gln Lys Tyr  
65 70 75 80

Ser Asn Ser Asn Tyr Tyr Phe Leu Ser Met Ala Val Trp Arg Asp Tyr  
85 90 95

Ile Thr Leu Glu Ser His Asp Leu Ala Glu Gly Tyr Thr Tyr Phe Phe  
100 105 110

Asn Glu Asn Thr Asp Asp Cys Tyr Val Leu Lys Gln Asp Phe Ile Asn  
115 120 125

Asn Glu Arg Tyr Glu Lys Thr Glu Leu Tyr Ser Gln Lys Asp Lys Val  
130 135 140

Ile Leu Phe Pro Lys Phe Gly Glu Tyr Asp Leu Val Leu Asn Pro Asp  
145 150 155 160

Ile Ile

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 acides aminés
- (B) TYPE : acide aminé
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

F04F39/2542550

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION:1..90

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

Met Asn Lys Arg Met Lys Met Cys Pro Ala Cys Gln Gln Gly Tyr Leu  
1                      5                      10                      15

Tyr His Ser Lys Pro Lys Tyr Leu His Asp Glu Ile Ile Leu Cys Asp  
                    20                      25                      30

Glu Cys Asp Ala Val Trp Leu Lys Gly Met Asn Ile Phe Tyr Gly Glu  
                    35                      40                      45

Tyr Glu Lys Asp Phe Tyr Ser Tyr Val Pro Phe Met Glu Ser Gln Gly  
                    50                      55                      60

Ile Thr Ser Glu Cys Ile Trp Glu Gly Asp Leu Phe Asp His Pro Tyr  
65                      70                      75                      80

Tyr Glu Asp Glu Asn Ser Asn Asp Met Asp  
                    85                      90

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 313 acides aminés

(B) TYPE : acide aminé

(C) STRANDEDNESS: single

(D) TOPOLOGY : linear

104400 2443260

(ix) **FEATURE:**

(B) LOCATION:1..313

Met Ser Ala Thr Glu Ile Glu Lys Ala Lys Ala Lys Ile Thr Ala Tyr  
1 5 10 15

Ser Lys Leu Val Ala Gly Thr Ala Ser Ala Val Val Gly Gly Asp Val  
20 25 30

Asn Thr Ala Ala Asn Ala Ala Gln Ile Ala Val Glu Asn Asn Thr Leu  
35 40 45

Tyr Pro Arg Cys Val Gly Ala Lys Cys Asp Glu Phe Gln Lys Glu Gln  
50 55 60

Gln Lys Trp Ile Arg Glu Asn Pro Glu Glu Tyr Arg Glu Val Leu Leu  
65                      70                      75                      80

Phe Gln Thr Gly Phe Ile Pro Ile Ile Gly Asp Ile Gln Ser Phe Val  
85 90 95

Gln Ala Gln Thr Ala Ala Asp His Leu Phe Ala Leu Leu Gly Val Val  
100 105 110

Pro Gly Ile Gly Glu Ser Ile Gln Ala Tyr Lys Val Ala Lys Ala Ala  
115 120 125

Lys Asn Leu Gln Gly Met Lys Lys Ala Leu Asp Lys Ala Ala Thr Val  
130 135 140

Ala Thr Ala Gln Gly Tyr Val Ser Lys Thr Lys Ile Lys Ile Gly Gln

145                      150                      155                      160  
 Thr Glu Leu Arg Val Thr Ala Ala Thr Asp Lys Gln Leu Leu Lys Ala  
                          165                      170                      175  
 Ile Gly Glu Gly Arg Asp Thr Thr Gly Lys Met Thr Glu Gln Leu Phe  
                          180                      185                      190  
 Asp Ser Leu Ala Lys Gln Asn Gly Phe Arg Val Leu Ser Gly Gly Lys  
                          195                      200                      205  
 Tyr Gly Gly Asn Asn Gly Phe Asp His Val Trp Gln Ala Ala Asp Gly  
                          210                      215                      220  
 Ser Val Val Leu Ile Val Glu Ser Lys Gln Ile Arg Asn Gly Thr Val  
                          225                      230                      235                      240  
 Gln Leu Asn Pro Asn Gly Ala Gly Gly Tyr Thr Gln Met Ser Glu Asp  
                          245                      250                      255  
 Trp Ile Arg Gln Val Leu Asp Gln Leu Pro Asp Gly Ser Pro Ala Lys  
                          260                      265                      270  
 Ala Ala Val Phe Lys Ala Asn Lys Asn Gly Thr Leu Lys Thr Ala Ile  
                          275                      280                      285  
 Ala Gly Val Asp Arg Gln Thr Gly Lys Ala Val Ile Leu Pro Val Lys  
                          290                      295                      300  
 Val Pro Ser Lys Thr Asn Ile Arg Arg  
                          305                      310

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 acides aminés
- (B) TYPE : acide aminé
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION:1..311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

Met	Gly	His	Asn	Met	Met	Thr	Thr	Gln	Lys	Trp	Tyr	Glu	His	Ile	Thr	1	5	10	15
Asn	Val	Ile	Ile	Gly	Asn	Thr	Ala	Asn	Phe	Asn	Ser	Gly	Cys	Leu	Asp	20	25	30	
Ser	Ile	Asp	Tyr	Val	Asp	Glu	Arg	Lys	Gly	Val	Pro	Leu	Ala	Ala	Met	35	40	45	
Gln	His	Ile	Phe	Met	Asp	Val	Arg	Ala	Ala	Ala	Ser	His	Ala	Tyr	Leu	50	55	60	
Phe	Glu	His	Asp	Leu	Lys	Lys	Phe	Lys	Gln	Tyr	Ala	Tyr	Val	Ala	Gly	65	70	75	80
Lys	Leu	Gly	Val	Leu	Leu	Ser	Val	Asn	Ser	Thr	Asp	Pro	Glu	Pro	Phe	85	90	95	
Phe	Phe	Pro	Cys	Asp	Met	Leu	Asn	Ile	Gln	Asn	Pro	Met	Phe	Leu	Met	100	105	110	
Leu	Met	Ser	Asp	Ser	Pro	Gln	Leu	Arg	Glu	Phe	Leu	Val	Arg	Asn	Ile	115	120	125	

F04T00" 45432660

Asp Asn Ile Ala Asn Asp Thr Glu Ala Phe Ile Asn Arg Tyr Asp Leu  
 130 135 140

Asn Arg His Met Ile Tyr Asn Thr Leu Leu Met Val Glu Gly Lys Gln  
 145 150 155 160

Leu Asp Arg Leu Lys Gln Arg Ser Glu Lys Val Leu Ala His Pro Thr  
 165 170 175

Pro Ser Lys Trp Leu Gln Lys Arg Leu Tyr Asp Tyr Arg Phe Phe Leu  
 180 185 190

Ala Phe Ala Glu Gln Asp Ala Glu Ala Met Lys Ala Ala Leu Glu Pro  
 195 200 205

Leu Phe Asp Lys Lys Thr Ala Arg Met Ala Ala Lys Glu Thr Leu Ser  
 210 215 220

Tyr Phe Asp Phe Tyr Leu Gln Pro Gln Ile Val Thr Tyr Ala Lys Ile  
 225 230 235 240

Ala Ser Met His Gly Phe Asp Leu Gly Ile Asp Gln Glu Ile Ser Pro  
 245 250 255

Arg Asp Leu Ile Val Tyr Asp Pro Leu Pro Ala Asp Glu Tyr Gln Asp  
 260 265 270

Ile Phe Asp Phe Met Lys Gln Tyr Asp Leu Ser Tyr Pro Tyr Glu Tyr  
 275 280 285

Leu Gln Asp Trp Ile Asp Tyr Tyr Thr Phe Lys Thr Asp Lys Leu Val  
 290 295 300

Phe Gly Asn Ala Lys Arg Glu  
 305 310

FOOTNOTES

## (2) INFORMATION FOR SEQ ID NO: 46:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

GCCACCGGTA CGGAAACTGA A

21

## (2) INFORMATION FOR SEQ ID NO: 47:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL : NO

## (iv) ANTISENSE : NO

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

CCTGAATTCA TGTCTATTCC ATTTTGAAGA

30

## (2) INFORMATION FOR SEQ ID NO: 48:

 090418 43432660  
 T04T00 43432660



## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

CCGAGATCTT TAACCCTTTG GGCTTAAGCG A

31

## (2) INFORMATION FOR SEQ ID NO: 49:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

GGGAGATCTC CCGCTCGTGT TGTGCATTA

29

T0429-242660

## (2) INFORMATION FOR SEQ ID NO: 50:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

AAGAGATCTG CAGCCAAGGC TCTCGAAA

28

## (2) INFORMATION FOR SEQ ID NO: 51:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

GGGAGATCTC AGGCTGCCGC CGTTGA

26

1047207342660

## (2) INFORMATION FOR SEQ ID NO: 52:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

GGGAGATCTC ACCCCAAGAA CGCCAAAA

28

## (2) INFORMATION FOR SEQ ID NO: 53:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

GGGAGATCTG AACGTATAGT AATCTATCCA A

31

F04T03A/2542660

## (2) INFORMATION FOR SEQ ID NO: 54:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

AGTGGCTCCT AG

12

## (2) INFORMATION FOR SEQ ID NO: 55:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

F04730-234360

AGCACTCTCC AGCCTCTCAC CGAG

24

## (2) INFORMATION FOR SEQ ID NO: 56:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

AGTGGCTCTT AA

12

## (2) INFORMATION FOR SEQ ID NO: 57:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

T04133 4542650

AGTGGCTGGC

10

## (2) INFORMATION FOR SEQ ID NO: 58:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

AGCACTCTCC AGCCTCTCAC CGAC

24

## (2) INFORMATION FOR SEQ ID NO: 59:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

T04130-4-23650

12

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTISENSE : NO

ACCGACGTCG ACTATCCATG AACG

24

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

GTACTTGCTT AA

12

(2) INFORMATION FOR SEQ ID NO: 62:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 base pairs

(B) TYPE : nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

GTACTTGGGC

10

(2) INFORMATION FOR SEQ ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE : nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

10-11-2019 10:10:10



(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

ACCGACGTCG ACTATCCATG AACC

24

(2) INFORMATION FOR SEQ ID NO: 64

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 base pairs

(B) TYPE : nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

AATTCTCCCT CG

12

(2) INFORMATION FOR SEQ ID NO: 65

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE : nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

104730-254663

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

AGGCAACTGT GCTATCCGAG GGAG

24

(2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 140 base pairs

(B) TYPE : nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

GATCAACTTT TCCCTGTTTG TCCCATACC GGTTTGAATG AACCGATTGC GCGCCGCGCG 60

TGTTGTTGGA CATTACCTGC GATTCAGACG GTACGATTGA CCACTACATC GAGGAGAACG 120

GCAATCAGGG TACAATGCTA 140

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 base pairs

(B) TYPE : nucleotide

T04T00 43422660

(D) TOPOLOGY : linear

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

CATCATCTAA ATTTGTCTTT ATTGGTTTTT ACGCCACTCA TTGCGGATAA ACAATATTCC 120

GCCTTGCCGT CGCGAATGTT CAAGCTAGCC TGCATCACCG TAATCAGGTT GCCCGTTACC 180

GAGCCTTCGA GA 192

(2) INFORMATION FOR SEQ ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 188 base pairs

(B) TYPE : nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

GATCCGGCTG CCGACGCGC GCAAAATTGC CGCCGAGGAA AGCGCGCACA ACCACGACGG 60

CAAAACCAGC GTATGGCAAT ACAAACATCT CGTGTTCCGT ACGGCAGGCA TTTTCTGCTA 120

TGTCGGCGCG GAGGTGTCTA TCGGTTCCGT GATGGTCAAC GTATTGGGTT ATCTGAAAGG 180

GCTGGATC 188

(2) INFORMATION FOR SEQ ID NO: 69:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 304 base pairs

(B) TYPE : nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

GATCCCCAC TTACCTCGG GCAGATTTTG CGCGTTCATT ACAATAGCGT ATTTATGCGT 60

TTGCGTTTGC GCTTGCCGCT GCGCGGTTATG GGAAAACATC AATATGGCGG 120

TATAAAGCGC GGTATGGCGG AAAACCTGCC GTTTCGAAGT TTTATTCATC TTTTATTCCT 180

TGAGTTTGCC TTCACGGGAC GGGGCGGCGC GCGGAACGCG GGGTTCGGTA AACCGCCCGA 240

TTCCGCGCCC GCCGAATTGC TGATTGAAAA GCTTACTTCC CCATTTTAAC TTTGCACACT 300

GATC 304

10472542550

## (2) INFORMATION FOR SEQ ID NO: 70:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

GATCAGACCC ATTTTCAGCG CACCGTAAGC GCGGATTTTC TCGAATTTTT CCAAAGCTGC	60
GGCATCGTTG TTGATGTCGT CTTGCAACTC TTTGCCCGTG TAGCCCAAGT CGGCGGCATT	120
CAGGAAAACG GTCGGAATGC CCGCGTTGAT GAGCGTGGCT TTCAAACGGC CTATATTCGG	180
CACATCAATT TCATCGACCA AATTGCCGGT TGGGAACATA CTGCCTTCGC CGTCGGCTGG	240
ATC	243

## (2) INFORMATION FOR SEQ ID NO: 71

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

F04T30/234E660

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

CGGCGGCGTA GTCCGCCGCG ACAGCGTTAC CATAAGCGGG ACAGACTACA CCCCTTTATC	60
TAACCCGCAA AGTTTGATA CGGAATTAAA ATGGTTGCTT CAAGAAGCTC CCGAAATAGA	120
AAATCCTTTC GACCGCGCCG TTTATCTCCA TAATAATTG GCGTATCTTC AATATTTTAA	180
AGATTGCAAT AAACGTACTG CCAGAACTG CATGACCTTG TCGCTGATGC GCTCCG	236

(2) INFORMATION FOR SEQ ID NO: 72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

CGGTCAATCA CAAGAAAGTC AGCCGTCTGA TGGCGAAGAC GGGGCTGAAG GCAGTGATAT	60
GGCGGCGCAA ATACCGCTCG TTCAAAGGAG AAGTCGGCAA AATTGCGCCG AATATCCTGC	120
GACGCTGTTT CCATGCAGAA AAGCCGAATG AGAAATGGGT AACGGACGTT GCCGAGTTCA	180
ATGTAGGCGG AGAAAAGATA TACCTTTCTC CGATTATGGA TTTGTTTAAC GGGGAAATCG	240

F04T80 4E42660

TCAGTTACCG TATTCAGACC CGCCCGACTT TCGATTGCGC

280

## (2) INFORMATION FOR SEQ ID NO: 73:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

CGGTCAGAAA CAGGCAAGGT AATGAAAATG CCTGAGGCAC GGACTGTGCT GCGAACGAAA 60

ACTCCTTACC GAAGTCTTCT ATACCCAGGC TCAATAGCCG CTCAAGGAGA GAGCTATCAT 120

## (2) INFORMATION FOR SEQ ID NO: 74:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

T04T00 4342660

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

CGGTCAGAAA CAGGCAAGGT AATGAAAATG CCTGAGGCAC GGACTGTGCT GCGAACGAAA 60

ACTCCTTACC GAAGTCTTCT ATACCCAGGC TCAATAGCCG CTCAAGGAGA GAGCTATCAT 120

## (2) INFORMATION FOR SEQ ID NO: 75:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 152 base pairs

(B) TYPE : nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

CGGTGTTTTT CTTAACAATT CGCCGACTTC ATGGCGATAT TTAAGTGACA GTTGCTCCGC 60

CCACGCAGTT GCGCCGAAC CAGCACCACG ACATTATACT GATTATGCAC ATCGGCAAGA 120

TCAAAC TGAC CTATCGTAGT ATCGCAGACT GT 152

## (2) INFORMATION FOR SEQ ID NO: 76

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 381 base pairs

(B) TYPE : nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY : linear

092457-0340  
F04T30-2342660



(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

CGGGAGGTTT TGTGCATCCT GATACCGATC GGTGTTGTT GCTCAAAGGA CAGAAGGCCG	60
CTGATAAACG AGATTACCTG TTTGTCGCTA TTGACGATTT TTATACTCTG CCATTTTGCC	120
AGACAAAACC GCAGACAGTG CTGCCAAGTT TCTGACCGAA CATCTGGCCG ACCCCTGCTT	180
GTACCTGATT GAGTACGCTT ACTCTGACAA TGATAGGTAA TATAAAGAGC CGTCCAACAT	240
GCTTTCGGTG CAGTTTGTTA TGATAATGGG ATTGGTTGGA GGCTTGCCCG ATTTGCTTGT	300
CCGCAGACCA ACGGTAAGGC GGAGCGGGTT ATCCGTACCT TGATGGAGAT GTGGCATGAG	360
GAACAGTCGT TTGACAGACC G	381

(2) INFORMATION FOR SEQ ID NO: 77

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 269 base pairs

(B) TYPE : nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

F04T99 4542260

CGGAGCATAA AATCGTTATT AAAGATAATG GTATAGGAAC GAGCTTCGAT GAAATCAATG 60  
 ATTTTATTTT GAGAATCGGT CGGAACAGAA GGGAAGAAAA ACAAGCCTCC CCGTGCGGAA 120  
 GAATTCCAAC GGGTAAAAAA GGCCTTGGTA AATTGGCATT ATTCGGGCTT GGCAACAAAA 180  
 TTGAAATTC TACTATCCAG GGAAACGAAA GGGTTACTTT TACTTTGGAT TATGCAGAGA 240  
 TTCGAAGAAG CAAGGGTATT TATCAACCG 269

(2) INFORMATION FOR SEQ ID NO: 78

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

CGGATGAAAA CGGCATACGC GCCAAAGTAT TTACGAACAT CAAAGGCTTG AAGATACCGC 60  
 ACACCTACAT AGAAACGGAC GCGAAAAAGC TGCCGAAATC GACAGATGAG CAGCTTTCGG 120  
 CGCATGATAT GTACGAATGG ATAAAGAAGC CCGAAAATAT CGGGTCTATT GTCATTGTAG 180  
 ATGAAGCTCA AGACGTATGG CCG 203

(2) INFORMATION FOR SEQ ID NO: 79:

T04T00/040600

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79

CGGTTTCAGG TTGTCGCGAA GGCTCGGTAA CGGGCAACCT GATTACGGGT GATGCAGGCA	60
GCTTGAACAT TCGCGACGGC AAGGCGGAAT ATGTTTATCC GCAATGAGTG GCGTAAAAAC	120
CAATAAAGAC AAATTTAGAT GATGTCGGGG AAGATGCCCCG ACCGACAAGA CTATGCAAAA	180
TATGAAAAAC CAAGTACGCG GATCAGGCAT GGATGCACGA TCCAATCCG	229

## (2) INFORMATION FOR SEQ ID NO: 80:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

T 0 4 4 3 3 4 2 2 6 6 0

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

```

CGGGTCGCTT TATTTTGTGC AGGCATTATT TTTCATTTT GGCTTGACAG TTTGGAAATA      60
TTGTGTATCG GGGGGGGGTA TTGCTGACG TAAAAAACTA TAAACGCCGC GCAAATATG      120
GCTGACTATA TTATTGACTT TGATTTTGTG CTGCGCGGTG ATGGATAAAA TCGCCAGCGA      180
TAAAGAATTT GCGAGAACCT GATGCCG                                           207

```

(2) INFORMATION FOR SEQ ID NO: 81 :

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 224 base pairs

(B) TYPE : nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

```

CGGCAACGAT TTGAGCTATC GCGGTTACGA CATTCTGGAT TTGGCACAAA AATGCCAGTT      60
TGAAGAAGTC GCCCACCTGC TGATTCACGG CCATCTGCCC AACAAATTCG AGCTGGCCGC      120
TTATAAAACC AAGCTCAAAT CCATGCGCGG CCTGCCTATC CGTGTGATTA AAGTTTTGGA      180
AAGCCTGCCT GCACATACCC ATCCGATGGA CGTAATGCGT ACCG                          224

```

(2) INFORMATION FOR SEQ ID NO: 82:

F04750-2342660

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

CGGGAACAGC CATTGCCCCAC GCCCACGCCC CCCAAGAAAG ACGGAAACTA CTGCCTAAAT 60

TTTCGGCAAT CAAGTTGACG ATTAAAGGGT TGGGGGCAGT TGCAGTAATA AACATAGCCG 120

ACGAAATGGG ATTGGAATGA TAGTTGACCA AAGCCAAATA TTTACCCATC TTGCCTTCTG 180

TGCCTTTTGC GGGATTGGAG CCGTAACTGC CG 212

## (2) INFORMATION FOR SEQ ID NO: 83

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83

104443 2542660

CGGGAATTCT GAGCAGAATG AAAGAAAGCA GGCTTGATAA TTTCATAAAG TTATTGGAAG 60

AAAAAGGATT TACCGTCCAT TTCGGTATTC ACAATACGGC TGATTACGGA ATTCCCCAAA 120

GCCGTAAAAG ATTTACGTTA ATTGCAAACA GAATAACCAA AGAAAAGCTG GAACCAGTCA 180

AGTATTCGGG CAAACGGCTT ACGGTAGCCG ATGTTTTGGG AATGGAAATG GCTTTCCCAA 240

CATTATTGCA GGACACCAAG ACGAAACGGA TTTTATGCAT AGCTGTGCGG GAATTATCTG 300

ATATCACTTG AACGATTGGC TTGATACCTA AAAACGGAGG AACCGTTGGC TTT 353

(2) INFORMATION FOR SEQ ID NO: 84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

AATCCGTAT CCAAACTTTG CGGGTTAGAT AAAGGGGTGT AGTCTGTCCC GCTTATGGTA 60

ACGCTGTGCG GCGGACTAC GCCCGGAGCC TTTTCCAGT AAGTTTTTCGG AAATCAGGCT 120

GTGGGTGGTT TTTAAGAAAT CCAACCAGTC AAACGGCTCG GGGCTGTCCA AACCGGACAC 180

AGGTGCCGGT AACTTTCCCT CAGGTTGATT AACATTACGG CATCCGAATA TAACTTCCCG 240

F04T00 254360

CCTGCGGTTT GCCCGAGTTT AAGCAATGCC TCGTATCGT ATTGATTATA AAGTGTTTCC 300

TTCCAATT 308

(2) INFORMATION FOR SEQ ID NO: 85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

AATTCGTGTG CCGCGTCGAC AAACCGCTGA CGTAGCGGAT GTCTCATGCC ACGTTTCAAA 60

GCAGGTTGAT GGCGGTTAGC AACCTCTGA TTCACTGGG ATAT 104

(2) INFORMATION FOR SEQ ID NO: 86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

104100 4542660

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

AATTGCGTAG AGTGGGCTTC AGCCACGTTT TTTCTTTTTC GGTCGTTGAT TGGTGGGCTG 60

AACCACTTGT TTCGGAAATC CGTATCATG 89

(2) INFORMATION FOR SEQ ID NO: 87:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 273 base pairs

(B) TYPE : nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

AATTTCCACC TATGCCCTAC GCAGCGATTA TCCGTGGTTT ACCCAAAGGG TGATTATGGC 60

AAAAGCGCGG GGTGAGCGA CCGCCTTTTG TTGCCGGCGT TCAAACGGGT TTTGATAGGA 120

AATGCAGGCA CGAAGCCTCG GCTGATTGTG ATGCACCTGA TGGGTTGCA CAGTGATTTT 180

TGCACACGTT TGGATAAGGA TCGCGGCGG TTTCAGTATC AAAGTAAAA AATATCCTGC 240

TATGTTTCCA TCAATCGCGC AAACCGATAA ATT 273

(2) INFORMATION FOR SEQ ID NO: 88:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 270 base pairs

1044790 1342660



- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

AATTCCTCCG CACGGGGAGG CTTGTTTTTC TTCCCTTCTG TTCCGACCGA TTCTCAAATA	60
AAAATCATTG ATTTTCATCGA AGTTCATTCC TATACCATTA TCTTTAATAA CGATTTTATG	120
CTCCGGTTTA TCGAATAACC TAACTTCCAC TTCCGTAGCA CATGCATCGT AGGCATTTCGC	180
TATCAACTCG GCAATCGCAG GAACAGTGTG CGAATACAAT CTTTACACCC AAATGTTTCGA	240
TTACGGTTGG CTCGAAACTC AATTTCAATT	270

(2) INFORMATION FOR SEQ ID NO: 89:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 267 base pairs
  - (B) TYPE : nucleotide
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

T04T00 234260

AATTATGAAC ACACGCATCA TCGTTTCGGC TCGTTTCGTT GCGTTGGCAT TAGCAGGTTG 60  
 CGGCTCAATC AATAATGTAA CCGTTTCCGA CCAGAACTT CAGGAACGTG CCGCGTTTGC 120  
 CTTGGGCGTC ACCAATGCCG TAAAAATCAG CAACCGCAGC AATGAAGGCA TACGCATCAA 180  
 CTTTACCGCA ACTGTGGGTA AGCGCGTGAC CAATGCTATG TTACCAGTGT AATCAGCACA 240  
 ATCGGCGTTA CCACTTCCGA TGCAATT 267

(2) INFORMATION FOR SEQ ID NO: 90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

AATTTTTATT TGGTTCGTAG TCATTTTGTG CAACTGAACG ATATTCGTTT TCATCATTGC 60  
 TAACGTCTAG TGCCCATTTGT GGCCCGTAAT AAGAGATTTT GTCTCCTTTT ACATGTTTGA 120  
 CGCTGACGGC ATACTGGGGA TCGATGACGG ATAATGTACG TCTGTTGACA TCTGCAACGC 180  
 TAAATCAATC ATCGGTATTG GATAATGCGT TGCCGATGTT TTGACTTGTA TGTT 234

(2) INFORMATION FOR SEQ ID NO: 91:

F04T80 434B2660

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 295 base pairs

(B) TYPE : nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

AAATCGGCCG GCTGTGTCAA ATAATGCGTT ACTTTGGCCG GGTCTTGTTT TTTGTAAGTG	60
GTGGTCTTTT TTTGCGCGTT ATCCCCATCT GTTTGAGTGC ATAGCAAATG GTGGCTGCCG	120
TACAATCAAA TGTTTGGCGT TCATGCAGAT AGGCATCATG GTGTTGCCCA ATATATTGAG	180
CCGGTTTTTG CCTATCCGAT TTGACGGCAT TTAGACCGGT AACTTGATGT TTTAAGCTGC	240
CTGTTTGTTC AAAGGCGAAT CCACAAGTAA AGCGTGTTTC TTGACAGGTT AAACG	295

## (2) INFORMATION FOR SEQ ID NO: 92:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 259 base pairs

(B) TYPE : nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

F04T39 434B55

AATTGTGTAT ATCAAGTAGG ATGGGCATTT ATGCCTGACC TACAAAACCA AAAACAACCT	60
ACCACCCTTA ATCAACTCCA CAAACCCTCT TCAGACAACC TCGTTTTTTTG AAAACAATC	120
TGTAAACAGA TAACTGCTGA AGAATACCGT TGCCGAGCCC CAAAACCCGT ACTGCAACTT	180
TTATTGTGAA CTTCCCATTA TGAGAAAATC CCTTTTCGTC CTCTTTCTGT ATTTCGTCCT	240
ACTTACTGCC AGCGAAATT	259

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

AATTGCACCA	CGCGATGATG	GGTACGCCTC	TGTTGCCATT	GCGACCGCCG	CCGCCGTGCC	60
CGGTACGCTG	GTCAACCTTG	CCGCGGCGGA	ACGGGTAAAG	AAGTGCGCTT	CGGGCATCCT	120
TCCGGTACAT	TGCGCGTCGG	TGCAGCGCCG	AATGTCAGGA	CGGACAATGG	ACGGCCACCA	180
AAGCGGTTAT	GAGCCGCAGC	GCACGCGTGA	TGATGGAAGG	TTGGGTCAGG	GTGCCGGAAG	240

(2) INFORMATION FOR SEQ ID NO: 94:

(A) LENGTH: 308 base pairs  
(B) TYPE : nucleotide  
(C) STRANDEDNESS: single  
(D) TOPOLOGY : linear

(iii) HYPOTHETICAL : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

(2) INFORMATION FOR SEQ ID NO: 95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

AATTCGGAGG AGCAGTACCG CCAAGCGTTG CTCGCCTATT CCGGCGGTGA TAAACAGAC	60
GAGGGTATCC GCCTGATGCA ACAGAGCGAT TACGGCAACT TGTCTACCA CATCCGTAAT	120
AAAAACATGC TTTTCATTTT TTCGGCAAGC AATGACGCAC AAGCTCAGCC CAACACAAC	180
GACCCTATTG CCATTTTATG AAAAAGACGC TCAAAAAGGC ATTATCACAG TTGCAGGCGT	240
AGACCGCAGT GGAGAAAAGT TCAATGGCTC CAACCATTGC GGAATT	286

(2) INFORMATION FOR SEQ ID NO: 96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

T04T30 2542650

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

AATTTGGATA CGTTGGAAAA GGGATATTTG ATTGGGAATG GGATGAAGAT AAGCGTAGAT 60  
 GAGTTGGGGA AAAAAGTGTT AGAACATATC GGTAAGAATG AACCGTTATT GTTGAAAAAT 120  
 CTACTGGTTA ACTTCAATCA GGGAAAACAT GAAGAAGTTA GGAAGTTGAT TTATCAGTTG 180  
 ATAGAGTTAG ATTTTCTGGA ACTTTTGTGA GGGATTCTAT GAAAACTGG AAGCAATT 238

## (2) INFORMATION FOR SEQ ID NO: 97:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL : NO

## (iv) ANTISENSE : NO

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

AATTCGGCAC GCAGGTTTTTC TAAAAAAGG CCGTTGATGA CTTTGTTCGAT ATTGGCGGCT 60  
 TCGGTGTAGT GCGCGCCCGC TTCGGCCGCT CTTGCGCGTC CATGACGGAT TGAAGAGCG 120  
 TGCCGAAGAT TTCTGGACTG ATGTTGCGCC AGTCGAAATT GCCGACACGG GAGGAATACC 180  
 TGCCAACAAG AGTGCAGGCA GCGTAATCAA ACCACCCCCA CCCGCAATCG CATCGATAAA 240  
 TCCGGCAATC ATCGCAACCA AACCCAAAGC GAGTATTATG TATAAATCTT CCATGTTTCT 300  
 TAATCCTGTT AACTTGCACC AA 322

F04T30 43423630

## (2) INFORMATION FOR SEQ ID NO: 98:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98

AATTTGTCGG CAATCTTCCC GGGTCGCTTT ATTTTGTGCA GGCATTATTT TTCATTTTTG 60  
 GCTTGACAGT TTGGAGATAT TGTGTATCGG GGGGGGGTAT TTGCTGACGT AAAAAACTAT 120  
 AAACGCCGCA GCAAAATATG GCTGACTATA TTATTGACTT TGATTTTGTC CTGCGCGGTG 180  
 ATGGATAAAA TCGCCAGCGA TAAAGATTTG CGAGAACCTG ATGCCGGCCT GTTGTGTAAT 240  
 ATTTTCGACC TGTAATTACG APTTGGCTTC CGCGCCGGCA CAATATGCCG CCAAGCGGCG 300  
 CCCACATTTT GGAAGC 316

## (2) INFORMATION FOR SEQ ID NO: 99:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 base pairs
- (B) TYPE : nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY : linear



(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL : NO

(iv) ANTISENSE : NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

AATTCGGACA GTATGAATAC AGCGGATTAA TACAAGGTAA GTTCATTACA ACGGAAAAAC	60
CTTTAAAGAA TAATATGAAA GGTATTACCT TGTTTGCCAA CGGGAATGGT AAATATGCCC	120
GAGTTTTTCA CTGAATAGCG AATCCAGCCA TTTCTATTCA TATTTGACTG GATGGCTGAA	180
TGTGGACTTT ATAGATAATG ACGATGAAGA TTAAATT	217

1047-2342660